

161745

Schreiber, David

From: Foley, Shanon
Sent: Tuesday, August 02, 2005 8:04 AM
To: Schreiber, David
Subject: 10/808964

Hi David. Please search nt SEQ ID NO: 2 and its complement. Please also include an interference search.

Thank you.
Shanon

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 01:25:13 ; Search time 5981 Seconds
(without alignments)

11283.723 Million cell updates/sec

Title: US-10-808-964A-2

Perfect score: 1773

Sequence: 1 ggtacctcgtgattgttc.....caaatcgccctcggtacc 1773

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	56.6	3.2	1101	9	CNS00LT2
c 2	50.2	2.8	939	9	AL078714 Drosophila
c 3	48.6	2.7	870	4	AL059400 Drosophila
c 4	48.2	2.7	573	6	BG445569 GA_Ea002
c 5	47.6	2.7	1141	9	CD659610 EtESTef53
c 6	47.4	2.7	922	9	AC365778 Mus muscu
c 7	46.6	2.6	571	6	AL066784 Drosophila
c 8	46.6	2.6	857	5	BP162319 BP162319
c 9	46.6	2.6	909	9	CA741621 wialc.pko
c 10	46.4	2.6	560	6	AL076720 Drosophila
c 11	46	2.6	401	2	CA222795 SCEZEL403
c 12	45.2	2.5	460	7	AW255252 pep
c 13	45.2	2.5	540	7	CV144191 EST955400
c 14	45.2	2.5	621	7	CV140472 EST951681
c 15	45.2	2.5	649	7	CV137364 EST948573
c 16	45.2	2.5	670	7	CV138441 EST949650
c 17	45.2	2.5	703	7	CN784300 EST782991
c 18	45.2	2.5	724	7	CV140340 EST951549
c 19	45.2	2.5	727	7	CV142163 EST953372
c 20	45.2	2.5	729	7	CV137577 EST948786
c 21	45.2	2.5	744	7	CV146884 EST958093
c 22	45.2	2.5	757	7	CO413802 EST944187
c 23	45.2	2.5	767	7	CO409276 EST939661
c 24	45.2	2.5	768	7	CO410601 EST940986
					CV138839 EST950048

c 25	45.2	2.5	769	7	CO413933
c 26	45.2	2.5	788	7	CV136509
c 27	45.2	2.5	788	7	CV141605
c 28	45.2	2.5	790	7	CO414433
c 29	45.2	2.5	790	7	CV139795
c 30	45.2	2.5	791	7	CO411407
c 31	45.2	2.5	793	7	CV139994
c 32	45.2	2.5	793	7	CV141902
c 33	45.2	2.5	806	7	CV147450
c 34	45.2	2.5	813	7	CV143480
c 35	45.2	2.5	818	7	CV140283
c 36	45.2	2.5	820	7	CV141069
c 37	45.2	2.5	826	7	CO414543
c 38	45.2	2.5	827	7	CV147922
c 39	45.2	2.5	830	7	CN784715
c 40	45.2	2.5	830	7	CN785819
c 41	45.2	2.5	830	7	CO410131
c 42	45.2	2.5	837	7	CV141290
c 43	45.2	2.5	845	7	CO411008
c 44	45.2	2.5	852	7	CV149200
c 45	45.2	2.5	855	7	CV148673

ALIGNMENTS

RESULT 1
CNS00LT2/c 1101 bp DNA linear GSS 14-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC:
DEFINITION BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL078714.1 GI:5102004
VERSION AL078714
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammos in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
source
1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR48P19"
/clone_lib="RPCI-98"
/note="end : TET3"
ORIGIN
Query Match 3.2%; Score 56.6; DB 9; Length 1101;
Best Local Similarity 21.6%; Pred. No. 0.00037;


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Qy 1101 CCTCTCCCGCACCTTC 1116
Db 265 CCACCTGCCACCGCTCC 250

RESULT 8
LOCUS BP162319
DEFINITION BP162319 full-length enriched swine cDNA library, adult thymus Sus
scrofa cDNA clone THY010093C05 5', mRNA sequence.
ACCESSION BP162319
VERSION BP162319
KEYWORDS BP162319.1 GI:40411792
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 857)
AUTHORS Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
Okumura,N., Hamabima,N. and Awata,T.
TITLE PEDE (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
JOURNAL Nucleic Acids Res. 32 (1), D484-D488 (2004)
COMMENT Contact: Hirohide Uenishi
National Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel.: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.
FEATURES
Location/Qualifiers
source 1..857
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="THY010093C05"
/tissue_type="thymus"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult
thymus"

ORIGIN
Query Match 2.6%; Score 46.6; DB 5; Length 857;
Best Local Similarity 57.0%; Pred. No. 0.23;
Matches 85; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 971 GGAGCGGTTCGCGAGAGAGACACCGCCCGCGAGCATCTTGGCGAGATCTTCGCC 1030
Db 212 GAAGCGCGCGCGCGCACCGAGCTCGCGCCACCGAAGCGCGCGCGCGCGCGCGCC 271

Qy 1031 GCCGCCCTGGCTGTCCACCGCCCGCGCATCTTGGAGAGGAAATGGCATCT 1090
Db 272 GCCACCGAAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 331

Qy 1091 TCAACACCGCGCTCTCCCGCACCTTCGGA 1119
Db 332 TCCGAGTGTGCTCTCCGCGAGTACTCA 360

RESULT 9
CNS00JTL/c
LOCUS CNS00JTL
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACK39G08 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL076720
VERSION AL076720.1 GI:4956298
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammossier in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
source 1..909
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACE39G08"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN
Query Match 2.6%; Score 46.6; DB 9; Length 909;
Best Local Similarity 22.6%; Pred. No. 0.23;
Matches 90; Conservative 118; Mismatches 190; Indels 0; Gaps 0;

Qy 1347 AACAAAGGCCACAGCCCTTAACCTATGACCCCATATGTAACACTCTCTCCGCCCATACAT 1406
Db 863 MAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMM 804

Qy 1407 CCCCCAACCCCTTCTCTACGACTCCGCTTACTTACACCCCAACCTGTTCTTGACTCCAC 1466
Db 803 MCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCM 744

Qy 1467 CATTGATTACTTCCAAACCAATAACAAAGAAATCAGCTTTGGATGAGGCTTACAAACCTC 1526
Db 743 CCCCCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCM 684

Qy 1527 TAGAAATGTGACACACCTAGGCTTCGGCCTTCGAAACACAGTATATACGACCGAGA 1586
Db 683 MAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMMAMM 624

Qy 1587 CTACAAATATCGGTGTAACCATGTATGTAATTCAGAGAAATTTAATCTTAAAGACCCCCC 1646
Db 623 ACMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCM 564

Qy 1647 ACTTAAACCCCTAAATGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1706
Db 563 AACCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCMCM 504

Qy 1707 GTAAATTTATTTATATATGGGAAAGGCGACAGGTGGGT 1744
Db 503 AMAAAAACAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAA 466
```

RESULT 10
CA222795/c
LOCUS
DEFINITION SCEZF14038H05.g FL4 Saccharum officinarum cDNA clone SCEZF14038H05
5', mRNA sequence.
ACCESSION CA222795
VERSION CA222795.1 GI:35278479
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.
REFERENCE 1 (bases 1 to 560)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bccccenter.fcav.unesp.br>
Plate: 038 row: H column: 05
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. .560
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCEZF14038H05"
/lab_host="DH10B"
/clone_lib="PL4"
/note="Organ: Developed inflorescence and rachis (20cm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from (developed inflorescence and rachis (20cm-long)). cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>"

FEATURES

source
1. .560

Query Match 2.6%; Score 46.4; DB 6; Length 560;
Best Local Similarity 58.0%; Pred. No. 0.24;
Matches 80; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
Qy 977 GTTACCGCAGAAAGACACCGCCCGCCAGCATCTTGCGCAGATCTCGCGCGCGCC 1036
Db 396 GGTCCG 337
Qy 1037 CCTGGCTGTCTCACCGCCCGCCAGCATCTTGCGCAGAAATGGCATCTTCAACA 1096
Db 336 GCTCCCTCCNCGCNCGCTCCACGACACACAGATCCGCGCCCGCGCTCCACCA 277
Qy 1097 CCGGCTCTCCGACCT 1114
Db 276 ACCACCTCCCGCACT 259

ORIGIN

Query Match 2.6%; Score 46.4; DB 6; Length 560;
Best Local Similarity 58.0%; Pred. No. 0.24;
Matches 80; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
Qy 977 GTTACCGCAGAAAGACACCGCCCGCCAGCATCTTGCGCAGATCTCGCGCGCGCC 1036
Db 396 GGTCCG 337
Qy 1037 CCTGGCTGTCTCACCGCCCGCCAGCATCTTGCGCAGAAATGGCATCTTCAACA 1096
Db 336 GCTCCCTCCNCGCNCGCTCCACGACACACAGATCCGCGCCCGCGCTCCACCA 277
Qy 1097 CCGGCTCTCCGACCT 1114
Db 276 ACCACCTCCCGCACT 259
RESULT 11
AW255252
LOCUS
DEFINITION ML252 peppermint glandular trichome Mentha x piperita cDNA, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW255252
AW255252.1 GI:7244504
EST.
Mentha x piperita (peppermint)
Mentha x piperita
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Lamiales; Lamiaceae; Nepetoideae; Nepeteae; Mentha.

REFERENCE

1 (bases 1 to 401)
AUTHORS Lange,B.M., Wildung,M.R., Stauber,E.J., Sanchez,C., Pouchnik,D. and Croteau,R.

TITLE

Probing essential oil biosynthesis and secretion by functional evaluation of expressed sequence tags from mint glandular trichomes

JOURNAL

MEDLINE

PUBMED

COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2934-2939 (2000)
20183992
10717007

FEATURES

source

Contact: Lange, B.M.
Institute of Biological Chemistry/Washington State University
Pullman, WA
Email: lange-m@mail.wsu.edu.
Location/Qualifiers
1. .401
/organism="Mentha x piperita"
/mol_type="mRNA"
/cultivar="Black Mitcham"
/db_xref="taxon:34256"
/tissue_type="peltate glandular trichomes"
/cell_type="secretory"
/clone_lib="peppermint glandular trichome"
/note="Vector: lambda ZAPII"

ORIGIN

Query Match 2.6%; Score 46; DB 2; Length 401;
Best Local Similarity 55.7%; Pred. No. 0.28;
Matches 88; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
Qy 959 TGACGTATCCAAGGAGCGTTACCGCAGAAAGACACCGCCCGCGGCGCATCTTGCC 1018
Db 126 TGGTTACTTACCTTCTCGCCACCAACCGCCATCGCCACCGCGCGGTGCTGCC 185
Qy 1019 AGATCTCCCGCGCGCCCTGGCTGTCTCCACCGCCCGACCGTTGGAGAGGA 1078
Db 186 GCATCCATCCGCTGACACCTCTGCTCCATCTCCACCGCCCGCGGTGCTGCGCTG 245
Qy 1079 ABAATGCGATCTTCAACACCGGCTCTCCGCGACCTTC 1116
Db 246 CCGCATCTCCGCGGACACCTCGGCTCCATCTCCATC 283

RESULT 12

CV144191/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CV144191
EST855400 Sequencing ESTs from loblolly pine embryos Pinus taeda
cDNA clone RP1D242 5' end, mRNA sequence.
CV144191
CV144191.1 GI:51906518
EST.
Pinus taeda (loblolly pine)
Pinus taeda
Pinus taeda

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 460)
Buell,C.R., Hsiao,J. and Cairney,J.
Sequencing of ESTs from loblolly pine embryonic libraries
Unpublished (2004)
Contact: C. Robin Buell
Plant Genomics Group
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: rbuell@tigr.org
This clone is available through TIGR. Please contact pine@tigr.org for further information

This clone is available through TIGR. Please contact pine@tigr.org for further information.

FEATURES

Location/Qualifiers

1. 540

/organism="Pinus taeda"

/mol_type="mRNA"

/cultivar="7-56 mother tree, open-pollinated tree from, Lyons, Georgia, USA"

/db_xref="taxon:3352"

/clone="rp1BR88"

/lab_host="E. coli DH10B-Tona"

/clone_lib="Sequencing ESTs from loblolly pine embryos"

/notes="Organ: Zygotic Embryo and Megagametophyte. Somatic Embryo; Vector: pCMV-SPORT 6.1; Site 1: NotI; Site 2: EcoRV; tissue: Whole megagametophytes isolated from pine seeds, Whole embryos excised from these megagametophytes, whole somatic embryos and suspensor tissue from tissue culture, isolated from cell line A12. Pooled RNA from zygotic embryos, megagametophytes, and somatic embryos was used for library construction. Pine cones were harvested weekly from open-pollinated 7-56 mother trees, collection occurred from 7/01/02 until 10/15/02. Whole megagametophytes were first isolated from pine seeds, and megagametophytes from these megagametophytes each with whole embryos excised from these megagametophytes were flash frozen. Embryo development was assessed using the system of Pullman et al (Pullman GS, Johnson S, Peter G, Cairney J, Xu N. 2003. Loblolly Pine Somatic embryogenesis: development of a maturation medium and resulting embryo quality. Plant Cell Reports 21:747-758 (<http://link.springer.de/link/service/journals/00299/content/03/00586/>). For photographs see Ciavatta et al 2001. (Ciavatta VT, Morillon R, Pullman GS, Christpeels M, Cairney J. 2001. An aquaglyceroporin is abundantly expressed early in the development of the suspensor and the embryo proper of loblolly pine (*Pinus taeda* L.). Plant Physiol. 127: 1556-1567 (<http://www.plantphysiol.org/cgi/content/full/127/4/1556>)

ORIGIN

	Query Match	2.5%	Score 45.2;	DB 7;	Length 460;
	Best Local Similarity	68.9%;	Pred. No. 0.49;		
	Matches 62;	Conservative 0;	Mismatches 28;	Indels 0;	Gaps 0;
Qy	980	ACGCGAGAGAGACACCGCCCCCGAGCCATCTTGGCCGAGATCTTCGCGCGCGCGCCCT	1039		
Db	280	ACGCGCGCGTAAACACCGCGCGTAGCCATCGCGCCTTCGCGCTACCGCGCGCTCG	221		
Qy	1040	GGCTGCTCACCCCGCGCACCGGTACGGTT	1069		
Db	220	GCCTCGGCTTCACACCGCTCCATGTT	191		

RESULT 14

LOCUS	CV140472	540 bp	mRNA	linear	EST 07-SEP-2004							
DEFINITION	EST951681 Sequencing ESTs from loblolly pine embryos Pinus taeda cDNA clone RPIBR88, mRNA sequence.											
ACCESSION	CV140472											
VERSION	CV140472.1	GI:51902793										
KEYWORDS	EST.											
SOURCE	Pinus taeda (loblolly pine)											
ORGANISM	Pinus taeda											
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 540)											
AUTHORS	Buell, C.R., Hsiao, J. and Cairney, J.											
TITLE	Sequencing of ESTs from loblolly pine embryonic libraries											
JOURNAL	Unpublished (2004)											
COMMENT	Contact: C. Robin Buell Plant Genomics Group The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: rbuella@tiqf.org											

CV137364/c	CV137364	621 bp	mRNA	linear	EST 07-SEP-2004							
LOCUS	EST948573	Sequencing ESTs from loblolly pine embryos Pinus taeda										
DEFINITION	CDNA clone RPIAN51 5' end, mRNA sequence.											
ACCESSION	CV137364											
VERSION	CV137364.1	GI:51899679										
KEYWORDS	EST.											
SOURCE	Pinus taeda (loblolly pine)											
ORGANISM	Pinus taeda											
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 621)											
AUTHORS	Buell,C.R., Hsiao,J. and Cairney,J.											
TITLE	Sequencing of ESTs from loblolly pine embryonic libraries											
JOURNAL	Unpublished (2004)											
COMMENT	Contact: C. Robin Buell Plant Genomics Group The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA											

Email: rbuell@tigr.org
This clone is available through TIGR. Please contact pine@tigr.org
for further information
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source

1. .621

/organism="Pinus taeda"
/mol_type="mRNA"
/cultivar="7-56 mother tree, open-pollinated tree from,
Lyons, Georgia, USA"
/db_xref="taxon:3352"
/clone="RPIAN51"
/lab_host="E.coli DH10B-Tona"
/clone_lib="Sequencing ESTs from loblolly pine embryos"
/note="Organ: Zygotic Embryo and Megagametophyte, Somatic
Embryo; Vector: pCMV-SPORT 6.1; Site 1: NotI; Site 2:
EcoRV; tissue: Whole megagametophytes isolated from pine
seeds, Whole embryos excised from these megagametophytes,
whole somatic embryos and suspensor tissue from tissue
culture, isolated from cell line A12. Pooled RNA from
zygotic embryos, megagametophytes, and somatic embryo was
used for library construction. Pine cones were harvested
weekly from open-pollinated 7-56 mother trees, collections
occurred from 7/01/02 until 10/15/02. Whole
megagametophytes were first isolated from pine seeds, and
whole embryos excised from these megagametophytes each was
flash frozen. Embryo development was assessed using the
system of Pullman et al (Pullman GS, Johnson S, Peter G,
Cairney J, Xu N. 2003. Loblolly pine somatic
embryogenesis: development of a maturation medium and
resulting embryo quality. Plant Cell Reports 21:747-758
http://link.springer.de/link/service/journals/00299/conte
nts/03/00586/). For photographs see Ciavatta et al 2001.
Clavatta VT, Morillon R, Pullman GS, Chrispeels M,
Cairney J. 2001. An aquaglyceroporin is abundantly
expressed early in the development of the suspensor and
the embryo proper of loblolly pine (Pinus taeda L.). Plant
Physiol. 127: 1556-1567
(http://www.plantphysiol.org/cgi/content/full/127/4/1556))

ORIGIN

Query Match 2.5%; Score 45.2; DB 7; Length 621;
Best Local Similarity 68.9%; Pred. No. 0.53;
Matches 62; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Qy 980 ACCGCGAAGAAGACACCGCCCGCAGCCATCTTGGCCAGATCCTCCGCGCGCCCT 1039
Db 308 ACCGCGCGGTAAACACCGCGCGGTAGCCATCGCGCTCTACGCGCGCTCG 249
Qy 1040 GGCTCGTCCACCGCGCCACCGTACCGTT 1069
Db 248 GCCTCGGCTCCACCGCGCTCCACTGTT 219

RESULT 15

CV138441/c
LOCUS
DEFINITION EST849650 Sequencing ESTs from loblolly pine embryos Pinus taeda
cDNA clone RPIB320 5' end, mRNA sequence.
CV138441
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Pinus taeda (loblolly pine)
Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 649)
Buell C.R., Hsiao J. and Cairney J.
Sequencing of ESTs from loblolly pine embryonic libraries
Unpublished (2004)
Contact: C. Robin Buell
Plant Genomics Group

The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: rbuell@tigr.org
This clone is available through TIGR. Please contact pine@tigr.org
for further information
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source

1. .649

/organism="Pinus taeda"
/mol_type="mRNA"
/cultivar="7-56 mother tree, open-pollinated tree from,
Lyons, Georgia, USA"
/db_xref="taxon:3352"
/clone="RPIB320"
/lab_host="E.coli DH10B-Tona"
/clone_lib="Sequencing ESTs from loblolly pine embryos"
/note="Organ: Zygotic Embryo and Megagametophyte, Somatic
Embryo; Vector: pCMV-SPORT 6.1; Site 1: NotI; Site 2:
EcoRV; tissue: Whole megagametophytes isolated from pine
seeds, Whole embryos excised from these megagametophytes,
whole somatic embryos and suspensor tissue from tissue
culture, isolated from cell line A12. Pooled RNA from
zygotic embryos, megagametophytes, and somatic embryos was
used for library construction. Pine cones were harvested
weekly from open-pollinated 7-56 mother trees, collections
occurred from 7/01/02 until 10/15/02. Whole
megagametophytes were first isolated from pine seeds, and
whole embryos excised from these megagametophytes each was
flash frozen. Embryo development was assessed using the
system of Pullman et al (Pullman GS, Johnson S, Peter G,
Cairney J, Xu N. 2003. Loblolly pine somatic
embryogenesis: development of a maturation medium and
resulting embryo quality. Plant Cell Reports 21:747-758
http://link.springer.de/link/service/journals/00299/conte
nts/03/00586/). For photographs see Ciavatta et al 2001.
Clavatta VT, Morillon R, Pullman GS, Chrispeels M,
Cairney J. 2001. An aquaglyceroporin is abundantly
expressed early in the development of the suspensor and
the embryo proper of loblolly pine (Pinus taeda L.). Plant
Physiol. 127: 1556-1567
(http://www.plantphysiol.org/cgi/content/full/127/4/1556))

ORIGIN

Query Match 2.5%; Score 45.2; DB 7; Length 649;
Best Local Similarity 68.9%; Pred. No. 0.53;
Matches 62; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Qy 980 ACCGCGAAGAAGACACCGCCCGCAGCCATCTTGGCCAGATCCTCCGCGCGCCCT 1039
Db 326 ACCGCGCGGTAAACACCGCGCGGTAGCCATCGCGCTCTACGCGCGCTCG 267
Qy 1040 GGCTCGTCCACCGCGCCACCGTACCGTT 1069
Db 266 GCCTCGGCTCCACCGCGCTCCACTGTT 237

Search completed: August 5, 2005, 06:31:56
Job time : 5981 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2005, 21:48:07 ; Search time 981 Seconds
(without alignments)
10698.982 Million cell updates/sec

Title: US-10-808-964A-2

Perfect score: 1773
Sequence: 1 ggtacctccgtgattgttc.....caaatcgcttcgggtacc 1773

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002as:*
7: Geneseq2002bs:*
8: Geneseq2003as:*
9: Geneseq2003bs:*
10: Geneseq2003cs:*
11: Geneseq2003ds:*
12: Geneseq2004as:*
13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1773	100.0	1773	9 AAL57177	Aal57177 Porcine c
c 2	1285.2	72.5	1768	6 ABX08205	Abx08205 PMWS-Porc
c 3	1278.8	72.1	1768	6 ABX08203	Abx08203 PMWS-Porc
c 4	1277.2	72.0	1768	6 ABX08207	Abx08207 CT-Porc
c 5	1274	71.9	1768	6 ABX08206	Abx08206 CT-Porc
c 6	1274	71.9	1768	6 ABX08204	Abx08204 PMWS-Porc
c 7	1270.8	71.7	1774	6 ABX08219	Abx08219 PMWS-Porc
c 8	1252	70.6	1762	6 ABX08202	Abx08202 PMWS-Porc
c 9	1218.2	68.7	1759	6 ABX08208	Abx08208 CT-Porc
c 10	1210.2	68.3	1759	6 ABX08220	Abx08220 PK-15-Porc
c 11	1196.8	67.5	7460	4 AAH74867	Aah74867 Nucleotid
c 12	1196.8	67.5	7460	8 ABX94361	Abx94361 Rolling c
c 13	1195.8	67.4	5285	4 AAH74865	Aah74865 Nucleotid
c 14	1195.8	67.4	5285	8 ABX94355	Abx94355 Rolling c
c 15	1195.8	67.4	5650	4 AAH74866	Aah74866 Nucleotid
c 16	1195.8	67.4	5650	8 ABX94356	Abx94356 Rolling c
c 17	1059.8	59.8	1759	4 AAF75839	Aaf75839 DNA fragm
c 18	1058.4	59.7	1768	9 AAL57176	Aal57176 Porcine c
c 19	1055.6	59.5	1759	2 AAX35013	Aax35013 Nucleotid
c 20	1053.2	59.4	3609	4 AAF28320	Aaf28320 pJP107 do

c 21	981.2	55.3	1768	2 AAX35380	Aax35380 Nucleotid
c 22	981.2	55.3	1768	2 AAX35212	Aax35212 Nucleotid
c 23	981.2	55.3	1768	3 AAZ56871	Aaz56871 DNA seque
c 24	981.2	55.3	1768	4 AAF75837	Aaf75837 PCV DNA f
c 25	976.4	55.1	1768	2 AAX35381	Aax35381 Nucleotid
c 26	976.4	55.1	1768	2 AAX35213	Aax35213 Nucleotid
c 27	976.4	55.1	1768	3 AAZ56872	Aaz56872 DNA seque
c 28	976.4	55.1	1768	2 AAX35382	Aax35382 PCV DNA f
c 29	967.2	54.6	1768	2 AAX35382	Aax35382 Nucleotid
c 30	967.2	54.6	1768	2 AAX35012	Aax35012 Genomic D
c 31	967.2	54.6	1768	2 AAX35214	Aax35214 Nucleotid
c 32	954	53.8	1767	2 AAX35378	Aax35378 Nucleotid
c 33	954	53.8	1767	2 AAX35210	Aax35210 Nucleotid
c 34	954	53.8	1767	3 AAZ56869	Aaz56869 DNA seque
c 35	954	53.8	1767	4 AAF75835	Aaf75835 PCV DNA f
c 36	952.4	53.7	1767	2 AAX35379	Aax35379 Nucleotid
c 37	952.4	53.7	1767	2 AAX35211	Aax35211 Nucleotid
c 38	952.4	53.7	1767	3 AAZ56870	Aaz56870 DNA seque
c 39	952.4	53.7	1767	4 AAF75836	Aaf75836 PCV DNA f
c 40	921	51.9	1759	2 AAX85593	Aax85593 Nucleotid
c 41	916.2	51.7	1759	2 AAX87992	Aax87992 Porcine c
c 42	742.2	41.9	1361	2 AAX83757	Aax83757 Porcine c
c 43	740.6	41.8	1786	2 AAX83755	Aax83755 Porcine c
c 44	738.4	41.6	1768	8 ABV72527	Abv72527 Nucleotid
c 45	725.6	40.9	1768	2 AAX83754	Aax83754 Porcine c

ALIGNMENTS

RESULT 1					
AAL57177					
ID	AAL57177 standard; DNA; 1773 BP.				
XX	AC AAL57177;				
XX	AC AAL57177;				
DT	27-OCT-2003 (revised)				
DT	09-OCT-2003 (first entry)				
XX	Porcine circovirus type 1-2 chimeric DNA.				
XX	Porcine circovirus type 2; PCV1-2; PCV1; PMWS; weaning piglet; dyspnoea;				
KW	progressive weight loss; postweaning multisystemic wasting syndrome; db;				
KW	tachypnea; anaemia; diarrhoea; jaundice; virucide; vaccine; PCV2; gene;				
KW	viral infection; chimeric.				
XX	Porcine circovirus type 1.				
OS	Porcine circovirus type 2.				
OS	Chimeric.				
Key	Location/Qualifiers				
CDS	958..1659				
FT	/*tag= a				
FT	/product= "Porcine circovirus type 2 ORF2 capsid protein"				
XX	WO2003049703-A2.				
XX	19-JUN-2003.				
XX	11-DEC-2002; 2002WO-US039646.				
XX	12-DEC-2001; 2001US-0340775P.				
PR	08-NOV-2002; 2002US-0424340P.				
PR	09-DEC-2002; 2002US-00314512.				
XX	(VIRG) VIRGINIA TECH INTELLECTUAL PROPERTIES.				
PA	(IOWA) UNIV IOWA STATE RES FOUND INC.				
XX	Meng X, Fenaux M, Halbur PG;				
XX	WPI; 2003-513959/48.				
DR	P-PSDB; AAO23063.				
XX					

PT New infectious chimeric nucleic acid molecule of porcine circovirus,
 PT useful for preventing and/or treating pigs against viral infection and/or
 PT postweaning multisystemic wasting syndrome.
 XX Claim 13; Fig 9; 85pp; English.

XX The invention relates to a novel infectious chimeric nucleic acid
 CC molecule of porcine circovirus (PCV1-2) which comprises a nucleic acid
 CC encoding an infectious, non-pathogenic PCV1 (porcine circovirus type 1)
 CC containing an immunogenic open 2) in place of a PCV1 ORF gene. Postweaning
 CC PCV2 (porcine circovirus type 2) is a complex disease of weaning
 CC multisystemic wasting syndrome (PMWS) is a complex disease of weaning
 CC piglets that is becoming increasingly more widespread. The condition
 CC poses a potentially serious economic threat to the swine industry, thus
 CC it has become important to develop a vaccine against PCV2, the primary
 CC causative agent of PMWS. PMWS mainly affects pigs between 5-18 weeks of
 CC age and clinical symptoms include progressive weight loss, dyspnoea,
 CC tachypnea, anaemia, diarrhoea and jaundice. The chimeric polynucleotide
 CC of the invention demonstrates virucide activity and may be utilised as a
 CC vaccine for PMWS. The methods and compositions of the present invention
 CC may be useful for the prevention and/or treatment of pigs against viral
 CC infection and/or PMWS. The current sequence is that of the PCV1-2
 CC chimeric DNA of the invention. (Updated on 27-OCT-2003 to standardise OS
 CC field)

XX SQ Sequence 1773 BP; 472 A; 511 C; 359 G; 431 T; 0 U; 0 Other;

Query Match		100.0%;	Score 1773;	DB 9;	Length 1773;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1773;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GGTACCTCCGCTGGATTCTCTCAGCAGTCTTCCAAATTTGCAAGTAGTAATCCTCCGA	60		
DB	1	GGTACCTCCGCTGGATTCTCTCAGCAGTCTTCCAAATTTGCAAGTAGTAATCCTCCGA	60		
QY	61	TAGAGAGCTTCTACAGCTGGGACAGCAGTGTGAGAGTACCATCTCTGGGGGGCTGATTG	120		
DB	61	TAGAGAGCTTCTACAGCTGGGACAGCAGTGTGAGAGTACCATCTCTGGGGGGCTGATTG	120		
QY	121	CTGGTAATCAAAATACATCGCGGCGCAAAAGGAACAGTACCCCTTTAGTCTCTACAGTC	180		
DB	121	CTGGTAATCAAAATACATCGCGGCGCAAAAGGAACAGTACCCCTTTAGTCTCTACAGTC	180		
QY	181	AATGGATACCGGTGACACAGTCTCAGTAGATCATCCCAAGTAAACAGCCATATAAATCA	240		
DB	181	AATGGATACCGGTGACACAGTCTCAGTAGATCATCCCAAGTAAACAGCCATATAAATCA	240		
QY	241	TCCAAAAACAACATCTTCTCCATGATATCCAFCCCAACATTAATTTCTATAGGCTTC	300		
DB	241	TCCAAAAACAACATCTTCTCCATGATATCCAFCCCAACATTAATTTCTATAGGCTTC	300		
QY	301	CAGTAGGTGCTCCCTAGCTCAGCAAAATAGGGGCGCCATGGCTCTTCCACACCGGGC	360		
DB	301	CAGTAGGTGCTCCCTAGCTCAGCAAAATAGGGGCGCCATGGCTCTTCCACACCGGGC	360		
QY	361	GGGCGCACTATGAGTGTACAGTGTCTCCAAATCAGCTGCTGCTCATCTTCCCGCTCACT	420		
DB	361	GGGCGCACTATGAGTGTACAGTGTCTCCAAATCAGCTGCTGCTCATCTTCCCGCTCACT	420		
QY	421	TTCAAAAAGTTGAGCGACCGCGGAAATTTCTCATATGTTTACAGGAAATCTGCTCGGCT	480		
DB	421	TTCAAAAAGTTGAGCGACCGCGGAAATTTCTCATATGTTTACAGGAAATCTGCTCGGCT	480		
QY	481	ACAGTACCAAGAACCCCGTCTCCAAAGGGTACTACAGCAGTACAGCGTCTGCTCGGC	540		
DB	481	ACAGTACCAAGAACCCCGTCTCCAAAGGGTACTACAGCAGTACAGCGTCTGCTCGGC	540		
QY	541	TTCCCTCGGTTCGCGGAGTCCACACTCGAATGATGTGGCCCTCTTTACTGCAATAT	600		
DB	541	TTCCCTCGGTTCGCGGAGTCCACACTCGAATGATGTGGCCCTCTTTACTGCAATAT	600		
QY	601	TCCTTATTCGCTGGTCCGTTCCCTTTCGATGTGGCAGCGGCAACCAAAATAC	660		

DB	601	TCCTTATTCGCTGGTCCGTTCCCTTTCGATGTGGCAGCGGGCAACCAAAATAC	660		
QY	661	CACCTCACCTTGTATAAAGTCTGCTCTTAGCAAAATTCGCAAAACCCCTGAGGTGAGGA	720		
DB	661	CACCTCACCTTGTATAAAGTCTGCTCTTAGCAAAATTCGCAAAACCCCTGAGGTGAGGA	720		
QY	721	GTTTCTACCTCTTCCAAACCTTCTCTCGCCAACAAACAAATAATCAAAAGGGAGATGGA	780		
DB	721	GTTTCTACCTCTTCCAAACCTTCTCTCGCCAACAAACAAATAATCAAAAGGGAGATGGA	780		
QY	781	AGCTCCGATATTTGTTTTTCTCTCTCGGAAGGATTAATTAAGGGTGAACACCCACTC	840		
DB	781	AGCTCCGATATTTGTTTTTCTCTCTCGGAAGGATTAATTAAGGGTGAACACCCACTC	840		
QY	841	TTATGGGTTGCGGGCGCTTTTCTTGTCTGGCAATTTCTACTGACGCTGCGGAGGTGCTG	900		
DB	841	TTATGGGTTGCGGGCGCTTTTCTTGTCTGGCAATTTCTACTGACGCTGCGGAGGTGCTG	900		
QY	901	CCGCTGCCGAAGTGCCTGGTAAATACACAGCAGCGCATCTTCTTCTATTTATAGGATG	960		
DB	901	CCGCTGCCGAAGTGCCTGGTAAATACACAGCAGCGCATCTTCTTCTATTTATAGGATG	960		
QY	961	ACGTATCCAAGGAGGGTACCCGAGAAAGACACCGCCCCCGCAGCCATCTTGGCCAG	1020		
DB	961	ACGTATCCAAGGAGGGTACCCGAGAAAGACACCGCCCCCGCAGCCATCTTGGCCAG	1020		
QY	1021	ATCCTCGCGCGCGCTCGCTCGCTCCACCCCGCCACCGCTACCGTTGGAGAAGAAA	1080		
DB	1021	ATCCTCGCGCGCGCGCTCGCTCGCTCCACCCCGCCACCGCTACCGTTGGAGAAGAAA	1080		
QY	1081	AATGGCATCTTCAACACCCGCTCTCCCGCACCTTGGATATCTGTCAAGGCTACCCACA	1140		
DB	1081	AATGGCATCTTCAACACCCGCTCTCCCGCACCTTGGATATCTGTCAAGGCTACCCACA	1140		
QY	1141	GTGAGAACCGCTCTCTGGGGGGTGAATGATGATTTAATTTGACGATTTGTTCCC	1200		
DB	1141	GTGAGAACCGCTCTCTGGGGGGTGAATGATGATTTAATTTGACGATTTGTTCCC	1200		
QY	1201	CCGGAGGGGGGACCAACAAATCTCTATACCTTTTGAATACTACAGAAATAAGAAAGTT	1260		
DB	1201	CCGGAGGGGGGACCAACAAATCTCTATACCTTTTGAATACTACAGAAATAAGAAAGTT	1260		
QY	1261	AAGTTGAAATTTCTGGCCCTCTCCCGCATCACCCAGGCTATAGGGAGTGGGCTCCACT	1320		
DB	1261	AAGTTGAAATTTCTGGCCCTCTCCCGCATCACCCAGGCTATAGGGAGTGGGCTCCACT	1320		
QY	1321	GCTGTTATTTCTAGATGATTAATTTGTAACAAAGGCGCACGCGCTTAACTATGACCCATAT	1380		
DB	1321	GCTGTTATTTCTAGATGATTAATTTGTAACAAAGGCGCACGCGCTTAACTATGACCCATAT	1380		
QY	1381	GTAACCTACTCTCCCGCCATACAAATCCCGCAACCCCTTCTCTACCACTCCCGTTACTTC	1440		
DB	1381	GTAACCTACTCTCCCGCCATACAAATCCCGCAACCCCTTCTCTACCACTCCCGTTACTTC	1440		
QY	1441	ACACCCAAACCTGTTCTTGACTCCACCATTTGATTTCTTCCAAACCAATAACAAAGGAAT	1500		
DB	1441	ACACCCAAACCTGTTCTTGACTCCACCATTTGATTTCTTCCAAACCAATAACAAAGGAAT	1500		
QY	1501	CAGTTTGGATGAGGTGACAAACCTCTAGAAATGTGACCAACCGTAGGCTCGGCACCTGCG	1560		
DB	1501	CAGTTTGGATGAGGTGACAAACCTCTAGAAATGTGACCAACCGTAGGCTCGGCACCTGCG	1560		
QY	1561	TTCCAAAACAGTATATACGACACGAGGACTACAAATCCGTTGTAACCATGTATGTACAAATTC	1620		
DB	1561	TTCCAAAACAGTATATACGACACGAGGACTACAAATCCGTTGTAACCATGTATGTACAAATTC	1620		
QY	1621	AGAGAAATTTAATCTTAAGACCCCGCTTAAACCTTAAATGAATAAATAAATAAATCCAT	1680		
DB	1621	AGAGAAATTTAATCTTAAGACCCCGCTTAAACCTTAAATGAATAAATAAATAAATCCAT	1680		
QY	1681	TACGATGTGATTAACAAAAGACTCAGTAATTTTATTTATATGGAAGGACACAGGT	1740		
DB	1681	TACGATGTGATTAACAAAAGACTCAGTAATTTTATTTATATGGAAGGACACAGGT	1740		

Qy 1741 GGGTCCACTGCTTCAAAATCGCCTTGGGTACC 1773
 Db 1741 GGGTCCACTGCTTCAAAATCGCCTTGGGTACC 1773

RESULT 2

ID ABX08205/c
 XX ABX08205 standard; DNA; 1768 BP.

AC ABX08205;

DT 20-JAN-2003 (first entry)

DE PMWS-Porcine circovirus (PCV) P4 genome.

XX Porcine circovirus genome; PCV; vaccine; type I PCV strain;
 KW type II PCV strain; congenital tremor; pig; whole PCV vaccine;
 KW passive immunisation; ds.

XX Porcine circovirus.

XX WO200196377-A2.

XX 20-DEC-2001.

XX 15-JUN-2001; 2001WO-US019220.

XX 15-JUN-2000; 2000US-0211710P.

XX (PURD) PURDUE RES FOUND.

XX Mittal SK, Stevenson GW, Choi J, Kiupel M, Kanitz CL;

XX WPI; 2002-106466/14.

XX New porcine circovirus (PCV) nucleic acids for use as a component of
 PT vaccines for treating or preventing congenital tremors in pigs.

XX Claim 1; Page 84; 88pp; English.

XX The invention describes an isolated nucleic acid (I) from a porcine
 CC circovirus (PCV) where (I) comprises a sequence coding for a circovirus
 CC polypeptide. A vaccine comprising a PCV nucleic acid that encodes an
 CC immunogenic polypeptide of type I or type II PCV strain and a carrier, is
 CC useful for treating or preventing congenital tremors in a pig or its
 CC progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II
 CC is composed of PMWS-PCV-P1, PMWS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).
 CC An isolated PCV strain (II) is useful for diagnosing a pathological cause
 CC of congenital tremors in a pig which involves determining whether the pig
 CC has been infected by PCV strain type I or type II. The determination of
 CC the infection is effected by detecting the presence of a PCV nucleic acid
 CC in a biological sample from the pig, by detecting hybridisation of an
 CC oligonucleotide. Optionally, the determination of infection is effected
 CC by detecting the presence of PCV polypeptide in a biological sample from
 CC the pig by detecting binding of an antibody that specifically binds a PCV
 CC polypeptide. Optionally, the determination of infection is effected by
 CC detecting the presence of antibodies directed against a PCV polypeptide
 CC in a biological sample of the pig. An expression vector (III) encoding a
 CC PCV polypeptide is useful as a vector vaccine against congenital tremors.
 CC (II) along with a suitable adjuvant is useful as a whole PCV vaccine,
 CC while the antigenic PCV polypeptides are used as components of subunit
 CC vaccines. Antibodies against PCV proteins are useful in passive
 CC immunisation strategies. This sequence represents a porcine circovirus
 CC genome

XX Sequence 1768 BP; 453 A; 358 C; 493 G; 464 T; 0 U; 0 Other;

Query Match 72.5%; Score 1285.2; DB 6; Length 1768;

Best Local Similarity 89.0%; Pred. No. 0;
 Matches 1462; Conservative 0; Mismatches 159; Indels 22; Gaps 6;

Qy 135 ACTCGGGGCCAAAAAAGGAACAGTACCCCTTTAGTCTCTACAGTCAATGGATACCGGTC 194

Db 1768 ACTCGGGGCCAAAAAAGGTACAGTTCCACCTTTTGTCTCTACAGTCAATGGATATCGATC 1709
 Qy 195 ACACAGTCTCAGTAGATCATCCCAAGGTAAACAGCATAAAAATCATCCAAAAACAAC 254
 Db 1708 ACACAGTCTCAGTAGATCATCCCAAGGTAAACAGCATAAAAATCATCAATCAACACCAC 1649
 Qy 255 TTCTTCTCCATGATATCATCCCAACCACTTATTTCTACTAGGCTTCCAGTGGTGTCCCT 314
 Db 1648 TTCTTCCACATGGTAAACCATCCCAACCACTTGTCTTAGTGGTGTTCAGTATGTGTTTC 1589
 Qy 315 AGGCTCAGCAAAATTAAGGGCCCACTGGCTCTTCCCAACAGGGGGGGCCCACTATGAC 374
 Db 1588 CGGGTCTGCAAAATTAAGCAGCCCAATTTGCTTTTACCAACCCAGGTGGCCCAACAATGAC 1529
 Qy 375 GTGTACAGAGTGTCTTCCAATCAGCTGTCTTCCCGCTCACTTCCCGCTCACTTTCAAAAGTTGAGC 434
 Db 1528 GTGTACATGGTCTTCCAAATCAGCTGTCTTCCCGCTCACTTCCCGCTCACTTTCAAAAGTTGAGC 1469
 Qy 435 CAGCCCGCGGAAATTTCTCACAATAGTTACAGGAACTGTCTGGCTACAGTCAACAAAGA 494
 Db 1468 CAGCCCGCGGAAATTTCTGACAAACGTTACAGGGTGTCTCTGCAACGGTCAACAGACT 1409
 Qy 495 CCGGCTCTCCAAAGGGTACTCAGCAGTAGACAGGTCTGGCTTCCCTTGGTTCGG 554
 Db 1408 CCGGCTCTCCAAAGGGTACTCAGCAGTAGACAGGTCTGGCTTCCCTTGGTTCGG 1349
 Qy 555 CGGAGCTCCACACTCGATATAGTGGCTTCTTACTGCAAGTATCTTTATTTCTGCTG 614
 Db 1348 AGGAGCTCCACATTCATTAAGTAAAGTTGCTTCTTACTGCAATATCTTTATTTCTGCTG 1289
 Qy 615 GTGGTTCCTTTTCGTTTCTGATGTGGCAGCGGCAACCAAAATACCACTTCACTTGT 674
 Db 1288 ATCAGTTCTTTGGCTTCTCGATGTGGCAGCGGCAACCAAAATACCACTTCACTTGT 1229
 Qy 675 AAAAGTCTGCTTCTTAGCAAAATTCGCAAAACCTTGGAGGTGAGAGTTCTACCTCTTC 734
 Db 1228 AAAAGTTCGCTTCTTCAAAATTAAGCAAAACCTTGGAGGTGAGGTGTTCGCTCTTCCTC 1169
 Qy 735 CAAACCTTCTCTCGCCACAAACAAATAATCAAAAGGAGATTCGAAAGCTCCCGTATTTT 794
 Db 1168 ATTACCTCTCTCGCCAAACAATAAATAATCAATAGGAGATTCGGAGCTCCCGTATTTT 1109
 Qy 795 GTTTTCTCTCTCGGAAGGATTTAAGGGTGAACACCCACTCTTATGGGTGCGG 854
 Db 1108 CTTGCGTCTGCTTTCGGAAGGATTTATCAGGTGAACACCCACTTTTATGTGGTTGGG 1049
 Qy 855 GCGGCTT-----TTCTGCTTGGCAATTTT-----CACTGACGCTCCGAGGTGCTGC 901
 Db 1048 TCCGCTTCTTCCATTTCTTGTGGGCAATGTTCTGCTGAGGTGCTGCCGAGGTGCTGC 989
 Qy 902 CGCTGCGAAGTGGCTGGTAATACTACAGCAGCGCACTTCTTTCACCTTTTATAGGATGA 961
 Db 988 CGCTGCGAAGTGGCTGGTAATACT--TACAGCGCACTTCTTTCGTTTTCA-GCTATGA 932
 Qy 962 CGTATCCAAGGAGCGTTACCGCAAGAAGACACCCGCCCGCAGCCATCTTGGCCAGA 1021
 Db 931 CGTATCCAAGGAGCGTTACCGCAAGAAGACACCCGCCCGCAGCCATCTTGGCCAGA 872
 Qy 1022 TCCTTCGCGCGGCCCTTGGCTGGTCCACCCCGCCACCGCTACCGTTGGAGAGAGAAA 1081
 Db 871 TCCTTCGCGCGGCCCTTGGCTGGTCCACCCCGCCACCGCTACCGTTGGAGAGAGAAA 812
 Qy 1082 ATGSCATCTTCAACACCCGCTCTCCCGCACTTTCGGATATACGTCAAGGCTACCCAG 1141
 Db 811 ATGGCATCTTCAACACCCGCTCTCCCGCACTTTCGGATATACGTCAAGGCTACCCAG 752
 Qy 1142 TCAGAACGCCCTCTCGGGCGGTGACATGATGAGATTTAATATTTGACGACTTTGTTCGCC 1201
 Db 751 TCACACGCCCTCTCGGGCGGTGACATGATGAGATTTAATATTTGACGACTTTGTTCGCC 692
 Qy 1202 CGGAGGCGGGGACCAACAAATCTCTATACCCCTTTGAATACTACAGAAATAAGAAGGTTA 1261

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Db 691 CGGAGGGGGACCAACAAAATCTCTATACCCTTTGAATACTACAGAATAAGAAAAGTTA 632
Qy 1262 AGGTTGAATTCGSCCTGCTCCCATCAACAGGGTGATAGGGAGTGGGTCCACTG 1321
Db 631 AGGTTGAATTCGSCCTGCTCCCATCAACAGGGTGATAGGGAGTGGGTCCACTG 572
Qy 1322 CTGTTATTTAGATGAATCTTGTAAACAAAGGCCACAGCCCTAAACCTATGACCCATATG 1381
Db 571 CTGTTATTTAGATGAATCTTGTAAACAAAGGCCCTCAGCCCTAAACCTATGACCCATATG 512
Qy 1382 TAAACTACTCTCCGCGCATACAAATCCCAACCCCTCTCTAGCACTCCCGTTACTTCA 1441
Db 511 TAAACTACTCTCCGCGCATACAAATCCCAACCCCTCTCTAGCACTCCCGTTACTTCA 452
Qy 1442 CACCCAACTGTTCTTGACTCCACCAATTCATTAATCTTCCCAACAAATAACAAAAGGAATC 1501
Db 451 CACCCAACTGTTCTTGACTCCACCAATTCATTAATCTTCCCAACAAATAACAAAAGGAATC 392
Qy 1502 AGCTTTGGATGAGCTACAAACCTCTAGAAATGTGGACCACTAGGCTCGGCACCTGCGT 1561
Db 391 AGCTTTGGATGAGCTACAAACCTCTAGAAATGTGGACCACTAGGCTCGGCACCTGCGT 332
Qy 1562 TCAGAAACAGTATATACGACGACGACTACAAATATCGGTGTAACCATGTATGTACAATTCA 1621
Db 331 TCAGAAACAGTATATACGACGACGACTACAAATATCGGTGTAACCATGTATGTACAATTCA 272
Qy 1622 GAGAAATTTAATCTTAAAGACCCCCACTTAAACCTTAAACCTTAAATGAATAAATAAACCATT 1681
Db 271 GAGAAATTTAATCTTAAAGACCCCCACTTAAACCTTAAACCTTAAATGAAT---AATAAACCATT 215
Qy 1682 ACAGTGTGATAACAAAAAGACTCAGTAATTTATTTTATATGGGAAAGGGCCACAGGGTG 1741
Db 214 ACAGAGTGAT---AAAAAGACTCAGTAATTTATTTTATATGGGAAATTCAGGGCATGGG 158
Qy 1742 GGTCCACTGCTTCAATTCGGCC 1763
Db 157 GGGAAAGGGTGACGAAGTGGCC 136
```

RESULT 3

ABX08203/c

ID ABX08203 standard; DNA; 1768 BP.

XX AC

AC AC

XX AC

XX AC

XX AC

XX AC

XX AC

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XX AC

XX AC

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XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

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XX AC

XX AC

XX AC

XX AC

XX Claim 1; Page 83; 88bp; English.

The invention describes an isolated nucleic acid (I) from a porcine circovirus (PCV) where (I) comprises a sequence coding for a circovirus polypeptide. A vaccine comprising a PCV nucleic acid that encodes an immunogenic polypeptide of type I or type II PCV strain and a carrier, is useful for treating or preventing congenital tremors in a pig or its progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II is composed of PMWS-PCV-P1, PMWS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6). An isolated PCV strain (II) is useful for diagnosing a pathological cause of congenital tremors in a pig which involves determining whether the pig has been infected by PCV strain type I or type II. The determination of the infection is effected by detecting the presence of a PCV nucleic acid in a biological sample from the pig, by detecting hybridisation of an oligonucleotide. Optionally, the determination of infection is effected by detecting the presence of PCV polypeptide in a biological sample from the pig by detecting binding of an antibody that specifically binds a PCV polypeptide. Optionally, the determination of infection is effected by detecting the presence of antibodies directed against a PCV polypeptide in a biological sample of the pig. An expression vector (III) encoding a PCV polypeptide is useful as a vector vaccine against congenital tremors. (II) along with a suitable adjuvant is useful as a whole PCV vaccine, while the antigenic PCV polypeptides are used as components of subunit vaccines. Antibodies against PCV proteins are useful in passive immunisation strategies. This sequence represents a porcine circovirus genome

XX Sequence 1768 BP; 452 A; 360 C; 496 G; 460 T; 0 U; 0 Other;

Query Match 72.1%; Score 1278.8; DB 6; Length 1768;

Best Local Similarity 88.8%; Pred. No. 0;

Matches 1458; Conservative 0; Mismatches 162; Indels 22; Gaps 6;

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Qy 135 ACTGCGGGCCAAAAGGACAGTACCCCTTTAGTCTCTACAGTCAATGGATACCGTTC 194
Db 1768 ACTGCGGGCCAAAAGGACAGTACCCCTTTAGTCTCTACAGTCAATGGATACCGTTC 1709
Qy 195 ACACAGTCTCAGTAGATCATCCCAAGTACACGACCATATAAAATATCCAAAACAAAC 254
Db 1708 ACACAGTCTCAGTAGATCATCCCAAGTACACGACCATATAAAATATCCAAAACAAAC 1649
Qy 255 TTCTTTCTCCATGATATCCATCCCACTTATTTCTACATAGGCTTCCAGTAGTGTCCCT 314
Db 1648 TTCTTTCTCCATGATATCCATCCCACTTATTTCTACATAGGCTTCCAGTAGTGTTC 1589
Qy 315 AGGCTCAGCAAAATTAAGGCGCCACTGGCTTCCACAGCGCGGGCCCATATGAC 374
Db 1588 CGGCTCTGCAAAATTAAGGCGCCACTGGCTTCCACAGCGCGGGCCCATATGAC 1529
Qy 375 GTGTACAGCTGTCTTCCAAATCAGCTGTCTGATCTTCCCGCTCACATTTCAAAAGTTCCAG 434
Db 1528 GTGTACATTTGCTTCTTCAATCAGCTTCTGATTTTCCCGCTCACATTTCAAAAGTTCCAG 1469
Qy 435 CAGCCCGCGGAAATTTCTCAATACGTTACAGGAAATGCTCGGCTACAGTCCACAAAGA 494
Db 1468 CAGCCCGCGGAAATTTCTGACAAACGTTACAGGCTGTCTCTGCAACGCTCCACGACT 1409
Qy 495 CCCGCTCTCCAAAGGGTACTCAGCAGTAGACAGTGTCTGGCTTCCCGCTGTTCOG 554
Db 1408 CCCGCTCTCCAAAGGGTACTCAGCAGTAGACAGTGTCTGGCTTCCCGCTGTTCOG 1349
Qy 555 CGGAGCTCCACACTCGATAGTATGTGGCTTCTTTACTGCAATATCTTTATTTCTGCTG 614
Db 1348 AGGAGCTCCACATTCATATAGTATGCTTCTTTACTGCAATATCTTTATTTCTGCTG 1289
Qy 615 GTCGGTTCTTTTCGCTTCTTCGATGTGGCAGCGGGCACCAAAATACACATTCACCTTGT 674
Db 1288 ATCAGTTCTTTTGGCTTCTTCGATGTGGCAGCGGGCACCAAAATACACATTCACCTTGT 1229
Qy 675 AAAAGTCTGCTTCTTAGCAAAATTCGCAAAATTCGAGGAGTGTCTTACCTCTTC 734
Db 1228 AAAAGTCTGCTTCTTAGCAAAATTCGCAAAATTCGAGGAGTGTCTTCTTCTTCTC 1169
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RESULT 4	
ID	ABX08207/c
XX	ABX08207 standard; DNA; 1768 BP.
XX	ABX08207;
XX	
DT	20-JAN-2003 (first entry)
XX	
DE	CT-Porcine circovirus (PCV) P6 genome.
XX	
KW	Porcine circovirus genome; PCV; vaccine; type I PCV strain;
KW	type II PCV strain; congenital tremor; pig; whole PCV vaccine;
KW	passive immunisation; ds.
XX	
OS	Porcine circovirus.
XX	
PN	W0200196377-A2.
XX	
PD	20-DEC-2001.
XX	
PF	15-JUN-2001; 2001WO-US019220.
XX	
PR	15-JUN-2000; 2000US-0211710P.
XX	
PA	(PURD) PURDUE RES FOUND.
XX	
PI	Mittal SK, Stevenson GW, Choi J, Kiupel M, Kanitz CL;
XX	
DR	WPI; 2002-106466/14.
XX	
DR	N-PSDB; ABU02906, ABU02911, ABU02922, ABU02929, ABU02935, ABU02942,
DR	ABU02948, ABU02955, ABU02960, ABU02966, ABU02968.
XX	
PT	New porcine circovirus (PCV) nucleic acids for use as a component of
PT	vaccines for treating or preventing congenital tremors in pigs.
XX	
PS	Claim 1; Page 85-86; 88pp; English.
XX	
CC	The invention describes an isolated nucleic acid (I) from a porcine
CC	circovirus (PCV) where (I) comprises a sequence coding for a circovirus
CC	polypeptide. A vaccine comprising a PCV nucleic acid that encodes an
CC	immunogenic polypeptide of type I or type II PCV strain and a carrier, is
CC	useful for treating or preventing congenital tremors in a pig or its
CC	progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II
CC	is composed of PWMS-PCV-P1, PWMS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).
CC	An isolated PCV strain (II) is useful for diagnosing a pathological cause
CC	of congenital tremors in a pig which involves determining whether the pig
CC	has been infected by PCV strain type I or type II. The determination of
CC	the infection is effected by detecting the presence of a PCV nucleic acid
CC	in a biological sample from the pig, by detecting hybridisation of an
CC	oligonucleotide. Optionally, the determination of infection is effected
CC	by detecting the presence of PCV polypeptide in a biological sample from
CC	the pig by detecting binding of an antibody that specifically binds a PCV
CC	polypeptide. Optionally, the determination of infection is effected by
CC	detecting the presence of antibodies directed against a PCV polypeptide
CC	in a biological sample of the pig. An expression vector (III) encoding a
CC	PCV polypeptide is useful as a vector vaccine against congenital tremors.
CC	(II) along with a suitable adjuvant is useful as a whole PCV vaccine,
CC	while the antigenic PCV polypeptides are used as components of subunit
CC	vaccines. Antibodies against PCV proteins are useful in passive
CC	immunisation strategies. This sequence represents a porcine circovirus
XX	genome
XX	
SQ	Sequence 1768 BP; 451 A; 362 C; 496 G; 459 T; 0 U; 0 Other;
	Query Match 72.0%; Score 1277.2; DB 6; Length 1768;
	Best Local Similarity 88.7%; Pred. No. 0;
	Matches 1457; Conservative 0; Mismatches 163; Indels 22; Gaps 6
Qy	135 ACTCGGGCCAAAAAGAACAGTAGTACCCCTTTAGTCTCTACAGTCAATGGATACCGGTC 194
Db	1768 ACTCGGGCCAAAAAGAGTACAGTTTCACCTTTAGTCTCTACAGTCAATGGATATCGATC 1705

Qy	195	ACACAGTCTCAGTAGATCATCTCCAGGTAAACGAGCCATAAAATCATCCAAAACAACAC	254
Db	1708	ACACAGTCTCAGTAGATCATCTCCAGCGCAGCAGCCATAAAAGATCATCAATAACAACAC	1649
Qy	255	TTCTTCTCCATGATATCCATCCCAACCACTTATTTCTACTAGGCTTCAGTAGGTGCCCT	314
Db	1648	TTCTTCCACCATGGTAACCATCCCAACCACTTGTTTCTAGGTGGTTTCAGATATGTGGTTT	1589
Qy	315	AGGCTCAGCAAAAATTACGGGCCCCACTGGCTCTTCCCAACAACCGGGGGGCCACTATGAC	374
Db	1588	CGGCTCTGCGAAATTAGCAGGCCATTTGCTTTTACACACCCAGGTGGCCCCCAATGAC	1529
Qy	375	GTGPAAGCTGTCTTCCAATCAGCGTCTGATCTTCCCGCTCACTTTCAAAAGTTGACG	434
Db	1528	GTGTACATTGGTCTTCCAATCAGCGTCTGCAATTTCCCGCTCACTTTCAAAAGTTGACG	1469
Qy	435	CAGCCCGGGNAATTTCTACATACGTTTACAGGAACTGTCTGGCTACAGTCAACCAAGA	494
Db	1468	CAGCCCGCGAAATTTCTGACAAACGTTTACAGGGTGTCTCTGCAACGGTCAACAGACT	1409
Qy	495	CCCGCTCTCCAAAAGGGTACTCACAGCAGTAGACAGGTCTGCTGGCTTCCCTCTGGTTCCG	554
Db	1408	CCCGCTCTCCAAAGGTAATCTCACAGCAGTAGACAGGTCACTCGTGTCTCTTGAGATCG	1349
Qy	555	CGGAGCTCCACACTCGATAAGTAGTGGCTTCTTTACTCGAGTATTTCTTTTATCTGTCTG	614
Db	1348	AGGAGCTCCCAATTCATAAGTAAGTTGCTTCTTTACTGCAATATTTCTTTTATCTGCTG	1289
Qy	615	GTGGTTTCCCTTTCGCTTTCTCGATGTGGCAGCGGGCACAAAATACCACTTCACCTTGT	674
Db	1288	ATCAGTTTCCCTTTGGCTTTCTCGATGTGGCAGCGGGCACCCAAATACCACTTCACCTTAT	1229
Qy	675	AAAAGTCTGCTTCTTAGCAAAATTCGCAAAACCCCTGAGAGTGAAGAGTCTTCCCTCTC	734
Db	1228	AAAAGTTTGTCTTTCACAAAATTAGCGAACCCCTGAGAGTGAAGTGTTCGCTCTCTC	1169
Qy	735	CAAACTTCTCTCGCACAAAACAAAATAATCAAAAAGGAGATTGGAAGTCCCGGTATTTT	794
Db	1168	ATTACCTCTCTCGCAACAATAAAATAATCAAAATAGGAGATTGGAGCTCCCGTATTTT	1109
Qy	795	GTTTTTCTCTCTCGAAGGATTTAAGGFTGAACACCCACTCTTATGGGGTGGCG	854
Db	1108	CTTTCGCTCGTCTTTTCGAAGGATTTATTCAGCGTGAACACCCACTTATTTGTGTGGG	1049
Qy	855	GCGCCTT-----TTCTTGTCTGGCATTTT-----CACTGACGCTGCGAGGTGCTGC	901
Db	1048	TCGCTTCTTCCATCTTCTTCTTGTGGGCATGTTGCTGCTGAGGTGCTGCGAGGTGCTGC	989
Qy	902	CGCTGCCGAAGTGCCTGGTAATACTACAGCAGCGCACTTTCTTTCACTTTTATAGGATGA	961
Db	988	CGCTGCCGAAGTGCCTGGTAAATACT--TACAGCGCACTTCTTTCTGTTTTCA-GCTATGA	932
Qy	962	CGTATCCAAGAGGCGTTACGGCAGAAGAAGACACGCGCCCGCGAGCCATCTTGGCCAGA	1021
Db	931	CGTATCCAAGAGGCGTTACGGCAGAAGAAGACACGCGCCCGCAGCCATCTTGGCCAGA	872
Qy	1022	TCCTTCGCGCGCCCTGCTGCTCGTCCACCCCGCCACCGCTACCGTTGAGAAGGAAAA	1081
Db	871	TCCTTCGCGCGCGCCCTGCTGCTCGTCCACCCCGCCACCGCTACCGTTGAGAAGGAAAA	812
Qy	1082	ATGGCATCTTCAACACCCGCTCTCCCGCACCTTCGGATATACTGTCAAGGCTACCAAG	1141
Db	811	ATGGCATCTTCAACACCCGCTTTCGCGACCTTTCGGATATACTGTCAAGGCTACCAAG	752
Qy	1142	TCGAAACGCTCTCTGGGCGGTGACATGATGATTTAATTTGACGACTTTTGTTCCTCC	1201
Db	751	TCGAAACGCTCTCTGGGCGGTGACATGATGATTTAAGCTTTTGAAGCTTTTGTTCCTCC	692
Qy	1202	CGGAGGGGGGACCAACAAATCTCTATACCTTTTGAATACTACAGAAATGAAGAAAGTTA	1261
Db	691	CGGAGGGGGGACCAACAAATCTCTATACCTTTTGAATACTACAGAAATGAAGAAAGTTA	632
Qy	1262	AGGTTGAATTTCTGGCCCTGCTCCCCCATCACCCAGGCTGATAGGGGAGTGGGCTCCACTG	1321

Db	631	AGSTTGAATCTGGCCCTGCTCCCCCATCACCGAGGTGATAGGGAGTGGGTCCCACTG	572
Qy	1322	CTGTATTCTTAGATGATAACTTTGTAAACAAGGCCACAGCCCTAACTATGACCCCATATG	1381
Db	571	CTGTATTCTTAGATGATAACTTTGTACCAAAAGGCCACAGCCCTAACTATGACCCCATATG	512
Qy	1382	TAAACTACTCTCTCCCGCCATACAAATCCCCCAACCCCTTCTGCTACCACTCCCGTTACTTCA	1441
Db	511	TAAACTACTCTCTCCCGCCACACAATCCCCCAACCCCTTCTGCTACCACTCCCGTTACTTCA	452
Qy	1442	CACCCAAACCTGTTCTTGACTCCACCAATTGATTACTTCCAAACCAAAATACAAAAGGAATC	1501
Db	451	CACCCAAACCTGTTCTTGACTCCCACTATTGATTACTTCCAAACCAAAATACAAAAGGAATC	392
Qy	1502	AGCTTTGGATGAGGCTACAAAACCTCTAGAAATGTGGACCACTGAGGCTCGGCACCTGCGT	1561
Db	391	AGCTTTGGCTGAGGCTACAAAACCTCTAGAAATGTGGACCACTGAGGCTCGGCACCTGCGT	332
Qy	1562	TCGAAACACGTATATACGACAGGACTACAAATATCCGTGTAAACATGTATGTACAATTCA	1621
Db	331	TCGAAACACGTATATACGACAGGACTACAAATATCCGTGTAAACATGTATGTACAATTCA	272
Qy	1622	GAGAAATTTAATCTTAAAGACCCGCCACTTAAACCCCTAAATGAATAAATAAATAAACCATT	1681
Db	271	GAGAAATTTAATCTTAAAGACCCGCCACTTAAACCCCTAAATGAATAAATAAATAAACCATT	215
Qy	1682	ACGATGTGATAACAAAAAGACTCAGTAATTTATTTATATGGAAAAAGGCACAGGGTG	1741
Db	214	ACGAGTGTAT--AAAAAGACTCAGTAATTTATTTATATGGAAAAAGGCATGGGG	158
Qy	1742	GGTCCACTGCTTCAAAATCGGCC	1763
Db	157	GGGAAAGGGTGACGAACTGGGCC	136
RESULT 5			
ABX08206/c			
ID ABX08206 standard; DNA; 1768 BP.			
XX	AC	ABX08206;	
XX	DT	20-JAN-2003 (first entry)	
XX	DE	CT-Porcine circovirus (PCV) P5 genome.	
XX	KW	Porcine circovirus genome; PCV; vaccine; type 1 PCV strain;	
XX	KW	type 11 PCV strain; congenital tremor; pig; whole PCV vaccine;	
XX	KW	passive immunisation; ds.	
XX	OS	Porcine circovirus.	
XX	PN	W0200196377-A2.	
XX	PD	20-DEC-2001.	
XX	PF	15-JUN-2001; 2001WO-US019220.	
XX	PR	15-JUN-2000; 2000US-0211710P.	
XX	PA	(PURD) PURDUE RES FOUND.	
XX	PI	Mittal SK, Stevenson GW, Choi J, Kiupel M, Kanitz CL;	
XX	DR	WPI; 2002-106466/14.	
XX	DR	N-PSDB; ABU02905, ABU02912, ABU02921, ABU02928, ABU02933, ABU02940,	
XX	DR	ABU02947, ABU02954, ABU02961, ABU02964, ABU02972.	
XX	PT	New porcine circovirus (PCV) nucleic acids for use as a component of	
XX	PT	vaccines for treating or preventing congenital tremors in pigs.	
XX	PS	Claim 1; Page 84-85; 88pp; English.	

CC The invention describes an isolated nucleic acid (I) from a porcine
 CC circovirus (PCV) where (I) comprises a sequence coding for a circovirus
 CC polypeptide. A vaccine comprising a PCV nucleic acid that encodes an
 CC immunogenic polypeptide of type I or type II PCV strain and a carrier, is
 CC useful for treating or preventing congenital tremors in a pig or its
 CC progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II
 CC is composed of PMS-PCV-P1, PMS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).
 CC An isolated PCV strain (II) is useful for diagnosing a pathological cause
 CC of congenital tremors in a pig which involves determining whether the pig
 CC has been infected by PCV strain type I or type II. The determination of
 CC the infection is effected by detecting the presence of a PCV nucleic acid
 CC in a biological sample from the pig, by detecting hybridisation of an
 CC oligonucleotide. Optionally, the determination of infection is effected
 CC by detecting the presence of PCV polypeptide in a biological sample from
 CC the pig by detecting binding of an antibody that specifically binds a PCV
 CC polypeptide. Optionally, the determination of infection is effected by
 CC detecting the presence of antibodies directed against a PCV polypeptide
 CC in a biological sample of the pig. An expression vector (III) encoding a
 CC PCV polypeptide is useful as a vector vaccine against congenital tremors.
 CC (II) along with a suitable adjuvant is useful as a whole PCV vaccine,
 CC while the antigenic PCV polypeptides are used as components of subunit
 CC vaccines. Antibodies against PCV proteins are useful in passive
 CC immunisation strategies. This sequence represents a porcine circovirus
 CC genome
 CC
 XX

SQ Sequence 1768 BP; 451 A; 361 C; 497 G; 459 T; 0 U; 0 Other;

Query Match 71.9%; Score 1274; DB 6; Length 1768;

Best Local Similarity 88.6%; Pred. No. 0;

Matches 1455; Conservative 0; Mismatches 165; Indels 22; Gaps 6;

Qy 135 ACTGGGCCCCAAAAGGAACAGTACCCCTTTAGTCTCTACAGTCAATGGATACCGGTC 194
 Db 1768 ACTGGGCCCCAAAAGGACAGTACAGTTCCACCTTTAGTCTCTACAGTCAATGGATACCGATC 1709
 Qy 195 ACACAGTCTCAGTAGATCATCCCAAGGTAAACGAGCCATAAAATCATCCAAACACACAC 254
 Db 1708 ACACAGTCTCAGTAGATCATCCCAAGGTAAACGAGCCATAAAAGTCAATCAACACACAC 1649
 Qy 255 TTCTTCTCCATGATATCCATCCACACCTATTTCTACTAGCTTCCAGTAGGTGTCCT 314
 Db 1648 TTCTTCCACATGGTAAACCATCCACCACTTGTCTAGGTGGTTCTCAGTAGTGGTTTC 1589
 Qy 315 AGGCTCAGCAAAATTAACGGGCCACTGGCTCTTCCCAACACGGGCGGCCCACTATGAC 374
 Db 1588 GGGGTCTGCAAAATTAAGCAGCCCAATTTGCTTTTACCAACACGAGTGCCCAACATGAC 1529
 Qy 375 GTGTACAGCTGTCTTCCAAATCAGCTGTGATCTTCCCGCTCAGTTTCAAAAGTTGAGC 434
 Db 1528 GTGTACATGTGTCTTCCAAATCAGCTGTGATCTTCCCGCTCAGTTTCAAAAGTTGAGC 1469
 Qy 435 CAGCCCGGGAAATTTCTCAGATAGTTTACAGGAAATGCTCGGCTACAGTCAACCAAGA 494
 Db 1468 CAGCCCGGGAAATTTCTCAGATAGTTTACAGGAAATGCTCGGCTACAGTCAACAGACT 1409
 Qy 495 CCGGCTCTCCAAAAGGGTACTCAGCAGTAGTACAGAGTGGCTTCCCGCTTCCCGTTCG 554
 Db 1408 CCGGCTCTCCAAAAGGGTACTCAGCAGTAGTACAGAGTGGCTTCCCGTTCGCTTGGATCG 1349
 Qy 555 CGGAGCTCCACATCTGATATGTGGCTTCTTTACTGAGTATTTCTTTATTTCTGCTG 614
 Db 1348 AGGAGCTCCCAATTAAGTAAAGTTGCTTCTTTACTGCAATATTTCTTTATTTCTGCTG 1289
 Qy 615 GTCCGTTCTTTCTGTTCTGATGTGGCAGCGGSCACCAAAATACCACTTCACTTGT 674
 Db 1288 ATCAGTCTCTTTGGCTTTCTGATGTGGCAGCGGSCACCAAAATACCACTTCACTTAT 1229
 Qy 675 AAAAGTCTGCTTCTTAGCAAAATTCGCAAAACCCCTGGAGGTGAGGAGTTCTACCCCTTC 734
 Db 1228 GAAAGTTTGTCTTCTTCAAAATTAGCGAACCCCTGGAGGTGAGGAGTTCTGCTTCTC 1169
 Qy 735 CAAACCTTCTCGCCCAACAAATATCAAAAGGGAGATTTGGAAGCTCCCGTATTTT 794

Db 1168 ATTACCTCTCTCGCCAAACAATAAATAAATAGGAGATTTGGAGCTCCCGTATTTT 1109
 Qy 795 GTTTTCTCTCTCGGAAGGATTTAAGGGTGAACACCCACCTCTCTTATGGGGTTGGG 854
 Db 1108 CTGGCTCGTCTTCGGAAGGATTTATCAGCGTGAACACCCACCTTTTATGTGGTGGG 1049
 Qy 855 GCGGCTT-----TTCCTTGTGGCATTTT-----CACTGACGCTGCGAGGTTGCTGC 901
 Db 1048 TCCGCTTCTTCCATTTCTTCTTGTGGGCATGTGTCTGTGAGGTCTGCGGAGGTGCTGC 989
 Qy 902 CGCTGCCGAAGTGGCTGTGTAATACTACAGCAGGCGCACTTCTTTCACATTTTATAGATGA 961
 Db 998 CGCTGCCGAAGTGGCTGTGTAATACT--TACAGCGCACTTCTTCTGTTTTCTA-GCTATGA 932
 Qy 962 CGTATCCAAGGAGGGTTTACCGCAGAGAAGACACCGCCCGCAGCCATCTTGGCCAGA 1021
 Db 931 CGTATCCAAGGAGGGTTTACCGCAGAGAAGACACCGCCCGCAGCCATCTTGGCCAGA 872
 Qy 1022 TCCTCCGCGCGCGCTGGCTGTGTCACCCCGCCGACCGCTACCGTTGGAGAGGAAAA 1081
 Db 871 TCCTCCGCGCGCGCTGGCTGTGTCACCCCGCCGACCGCTACCGTTGGAGAGGAAAA 812
 Qy 1082 ATGCGCATCTTCAACACACCGCGCTCTCCGCACTTCCGATATATCTCAAGGCTACACAG 1141
 Db 811 ATGCGCATCTTCAACACACCGCGCTCTCCGCACTTCCGATATATCTCAAGGCTACACAG 752
 Qy 1142 TCAGAACGCGCTCTCTGGGCGGTGGACATGATGAGATTTAATATTGACGACTTTTGTCCCC 1201
 Db 751 TCAGAACGCGCTCTCTGGGCGGTGGACATGATGAGATTTAAGCTTGACGACTTTTGTCCCC 692
 Qy 1202 CGGAGGAGGGGACCAAAATCTCTATACCCCTTTGAAATATCTACAGAAATAGAAAGTTA 1261
 Db 691 CGGAGGAGGGGACCAAAATCTCTATACCCCTTTGAAATATCTACAGAAATAGAAAGTTA 632
 Qy 1262 AGGTTGAATCTGCGCTGCTCCCACTCACCCAGGGTGATAGGGAGTGGGCTCCACTG 1321
 Db 631 AGGTTGAATCTGCGCTGCTCCCACTCACCCAGGGTGATAGGGAGTGGGCTCCACTG 572
 Qy 1322 CTGTTATTTCTAGATGATAAATCTTTGTAAACAAAGGGCCACAGCCCTAACCTATGACCCATATG 1381
 Db 571 CTGTTATTTCTAGATGATAAATCTTTGTACCAAGGCCAATGCGCTTACCTATGACCCATATG 512
 Qy 1382 TAAACTACTCTCCGCGCATCAATCCCGCCCAACCCCTTCTCTCTACCACTCCCGTTACTTCA 1441
 Db 511 TAAACTACTCTCCGCGCATCAATCCCGCCCAACCCCTTCTCTCTACCACTCCCGTTACTTCA 452
 Qy 1442 CACCCAAACCTGTTCTTGACTCCACCTTGATTTACTTCCAACTCAAAATTAACAAAGGAATC 1501
 Db 451 CACCCAAACCTGTTCTTGACTCCCACTTTGATTTACTTCCAACTCAAAATTAACAAAGGAATC 392
 Qy 1502 AGCTTTGGATGAGGCTACAAACCTCTAGAAATGTGGACACAGTAGGCGCTCGGCACTGGGT 1561
 Db 391 AGCTTTGGATGAGGCTACAAACCTCTAGAAATGTGGACACAGTAGGCGCTCGGCACTGGGT 332
 Qy 1562 TCGAAAAACAGTATATACGACAGGACTACAAATATCCCGTGTAAACCATGTATGTACAAATCA 1621
 Db 331 TCGAAAAACAGTATATACGACAGGACTACAAATATCCCGTGTAAACCATGTATGTACAAATCA 272
 Qy 1622 GAGAAATTAATCTTAAAGACCCCGCACTTAAACCTTAAATGAATAAATAAATAAACCATT 1681
 Db 271 GAGAAATTAATCTTAAAGACCCCGCACTTAAACCTTAAATGAATAAATAAATAAACCATT 215
 Qy 1682 ACAGTGTGATAACAAAAAGACTCAGTAAATTTATTTTATATGGGAAAGGGCACAGGGTG 1741
 Db 214 ACAGTGTGAT---AATAAGACTCAGTAAATTTATTTTATATGGGAAAGGGCACAGGGTG 158
 Qy 1742 GGTCCACTGTCTCAAAATCGGCC 1763
 Db 157 GGGAAAGGGTGAACAACTGGCC 136

RESULT 6
 ABX08204/c

Db 1642 TTCTTACCATGGTAAACCATCCACCATCTGTTTCTAGTGGTTTCCAGTANGTGTTTC 1583
Qy 315 AGGCTCAGCAAAATTAACGGGCCCACTGGCTCTTCCACAAACGGGGCCCACTATGAC 374
Db 1582 CGGGTCTGCAAAATTAAGCAGCCATTGCTTTTACCAACACGAGTGGCCCAATGAC 1523
Qy 375 GTGTACAGCTGTCTTCCAAATCAGCTGTGCAATCTTCCGCTCACTTTCAAAAGTTGAC 434
Db 1522 GTGTACATGTGTTTCCAAATCAGCTGTGCAATCTTCCGCTCACTTTCAAAAGTTGAC 1463
Qy 435 CAGCCCGGGGAAATTTCTCACATACGTTTACAGGAAATCTGCTGGCTCAGTCAACCAAGA 494
Db 1462 CAGCCCGGGGAAATTTCTGCAAAAGTTTACAGGGTGTGCTCTGCAACGGTCAACGACT 1403
Qy 495 CCGCGTCTCCAAAGGGTACTCACAGCAGTAGACAGGTGCTGCGCTTCCCGTTCGG 554
Db 1402 CCGCGTCTCCAAAGGGTACTCACAGCAGTAGACAGGTGCTGCGTTCGCTTGGATCG 1343
Qy 555 CGGAGCTCCACACTCGATAAGTATGTGGCTTCTTACTGCAATTTCTTATTTCTGCTG 614
Db 1342 AGGAGCTCCACATTCAAATGAAGTGTGCTTCTTACTGCAATTTCTTATTTCTGCTG 1283
Qy 615 GTGCGTTCCTTTGCTTTCTGATGTGGCAGCGGCACCAAAATACCACTTTCACCTGTT 674
Db 1282 ATCAGTTCCTTTGCTTTCTGATGTGGCAGCGGCACCAAAATACCACTTTCACCTTAT 1223
Qy 675 AAAAGTCTGCTTTCTAGCAAAATTCGAAACCCCTGGAGGTGAGAGTTTACCCCTCTC 734
Db 1222 AAAAGTTCCTTTCTTACAAATTAGCGAACCCCTGGAGGTGAGGTGTTCTGCTCTC 1163
Qy 735 CAAACCTTCCTGCGCAAAACAAATTAATCAAAAGGGAGATTGGAAGCTCCCGTATTTT 794
Db 1162 ATTACCTCTCTCGCCAAACAATAAATAATCAATAGGGAGATTGGGAGCTCCCGTATTT 1103
Qy 795 GTTTTCTCTCTCTCGGAGGATTATTAAGGTGGAACCCACCTCTTATGSGGTGGG 854
Db 1102 ATTGGCTCGTCTCGGAGGATTATTCAGGTGAACCCACCTTTTATGTGGTGGG 1043
Qy 855 GCGGCTT-----TTCCTGCTTGGCAATTT-----CACTGACGCTGCCAGGTGCTGC 901
Db 1042 TCCGCTTCTTCCATTTCTTGTGCGGCATGTGCTGTGAGGTGCTGCGAGGTGCTGC 983
Qy 902 CGTGTCCGAAGTGGCTGGTAATTAATAACAGCGCACTTCTTCACTTTTATAGTAGA 961
Db 982 CGTGTCCGAAGTGGCTGGTAATACT--TACAGCGCACTTCTTTC-GTTTTCAGCTAGA 926
Qy 962 CGTATCCAGGAGCGTTTACCGCAGAGAGACACACCGCCCGCAGCATCTTGGCCAGA 1021
Db 925 CGTATCCAGGAGCGTTTACCGCAGAGAGACACCGCCCGCAGCATCTTGGCCAGA 866
Qy 1022 TCCTCCGCGCGCGCCCTGCTGCTCCACCCCGCCACCGCTACCGTTGGAGAGAGAAA 1081
Db 865 TCCTCCGCGCGCGCCCTGCTGCTCCACCCCGCC-----ACGTTGGAGAGAGAAA 812
Qy 1082 ATGGATCTTCAACACCGCGCTCTCCGCACTTCCGATATCTGTCAAGGCTACCAAG 1141
Db 811 ATGGATCTTCAACACCGCGCTCTCCGCACTTCCGATATCTGTCAAGGCTACCAAG 752
Qy 1142 TCAGAGCCCTCTCTGGCGGTGACATGATGATTTAATTTGACGACTTTGTTCCCC 1201
Db 751 TCAACAGCCCTCTGGCGGTGACATGATGATTTAAGCTTTGACGACTTTGTTCCCC 692
Qy 1202 CGGAGGGGGGACCAACAAATCTCTATACCTTTTGAATCTACAGATAAGAAAGTTA 1261
Db 691 CGGAGGGGGGACCAACAAATCTCTATACCTTTTGAATCTACAGATAAGAAAGTTA 632
Qy 1262 AGGTTGAATTTGCGCTGCTCCCGCATCAACCGAGGTGATAGGGAGTGGCTTCCATG 1321
Db 631 AGGTTGAATTTGCGCTGCTCCCGCATCAACCGAGGTGATAGGGAGTGGCTTCCATG 572
Qy 1322 CTGTTATCTAGATGATTAATTTGTAACAAAGGCCACGCGCTAACCTATGACCCATATG 1381
Db 571 CTGTTATTTCTAGATGATTAATTTGTAACAAAGGCCAATGCGCTTAACCTATGACCCATATG 512

RESULT 9

ABX08208/c

ID ABX08208 standard; DNA; 1759 BP.

XX AC ABX08208;

XX XX

XX DT 20-JAN-2003 (first entry)

XX XX

XX DE CT-Porcine circovirus (PCV) P7 genome.

XX XX

XX KW Porcine circovirus genome; PCV; vaccine; type I PCV strain;

XX KW type II PCV strain; congenital tremor; pig; whole PCV vaccine;

XX KW passive immunisation; ds.

XX XX

XX OS Porcine circovirus.

XX XX

XX PN WO200196377-A2.

XX XX

XX PD 20-DEC-2001.

XX XX

XX PF 15-JUN-2001; 2001WO-US019220.

XX XX

XX PR 15-JUN-2000; 2000US-0211710P.

XX XX

XX PA (PURD) PURDUE RES FOUND.

XX XX

XX PI Mittal SK, Stevenson GW, Choi J, Kiupel M, Kanitz CL;

XX XX

XX XX WPI; 2002-106466/14.

XX DR

XX XX New porcine circovirus (PCV) nucleic acids for use as a component of

XX XX vaccines for treating or preventing congenital tremors in pigs.

XX PT

XX XX

XX PS Claim 1; Page 86; 88pp; English.

XX XX

XX CC The invention describes an isolated nucleic acid (I) from a porcine

XX CC circovirus (PCV) where (I) comprises a sequence coding for a circovirus

XX CC polypeptide. A vaccine comprising a PCV nucleic acid that encodes an

XX CC immunogenic polypeptide of type I or type II PCV strain and a carrier, is

XX CC useful for treating or preventing congenital tremors in a pig or its

XX CC progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II

XX CC is composed of PMWS-PCV-P1, PMWS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).

XX CC An isolated PCV strain (II) is useful for diagnosing a pathological cause

CC of congenital tremors in a pig which involves determining whether the pig
CC has been infected by PCV strain type I or type II. The determination of
CC the infection is effected by detecting the presence of a PCV nucleic acid
CC in a biological sample from the pig, by detecting hybridisation of an
CC oligonucleotide. Optionally, the determination of infection is effected
CC by detecting the presence of PCV polypeptide in a biological sample from
CC the pig by detecting binding of an antibody that specifically binds a PCV
CC polypeptide. Optionally, the determination of infection is effected by
CC detecting the presence of antibodies directed against a PCV polypeptide
CC in a biological sample of the pig. An expression vector (III) encoding a
CC PCV polypeptide is useful as a vector vaccine against congenital tremors.
CC (ii) along with a suitable adjuvant is useful as a whole PCV vaccine,
CC while the antigenic PCV polypeptides are used as components of subunit
CC vaccines. Antibodies against PCV proteins are useful in passive
CC immunisation strategies. This sequence represents a porcine circovirus
CC genome
XX

Seq	Sequence	1759 BP;	430 A;	347 C;	508 G;	474 T;	0 U;	0 Other;
Query Match	68.78;	Score	1218.2;	DB	6;	Length	1759;	
Best Local Similarity	85.28;	Pred. No.	0;					
Matches 1402;	Conservative	0;	Mismatches	223;	Indels	20;	Gaps	3;
Qy	135	ACTGCGGCCCCAAAGAAAGGACAGTACCCCTTTAGTCTCTACAGTCAATGGATACCGGTC	194					
Db	1759	ACTGCGGCCCCAAAGAAAGGACAGTACCCCTTTAGTCTCTACAGTCAATGGATACCGGTC	1700					
Qy	195	ACACAGTCTCAGTAGATCATCCCAAGGTAAACGCCATAAATATCATCCAAACAAAC	254					
Db	1699	ACACAGTCTCAGTAGATCATCCCAAGGTAAACGCCATAAATATCATCCAAACAAAC	1640					
Qy	255	TTCTTCTCCATGATATCCATCCACCACTTATTTCTACTAGGCTTCCAGTAGGTGCCT	314					
Db	1639	TTCTTCTCCATGATATCCATCCACCACTTATTTCTACTAGGCTTCCAGTAGGTGCCT	1580					
Qy	315	AGGCTCAGCAAAATTAACGGGCCCACTGGCTCTTCCCAACACCGGGCGGCCCATATGAC	374					
Db	1579	AGGCTCAGCAAAATTAACGGGCCCACTGGCTCTTCCCAACACCGGGCGGCCCATATGAC	1520					
Qy	375	GTGTACAGTGTCTTCAATCAACGCTGTGATCTTCCCGGTCACTTTTCAAAAGTTTCAGC	434					
Db	1519	GTGTACAGTGTCTTCAATCAACGCTGTGATCTTCCCGGTCACTTTTCAAAAGTTTCAGC	1460					
Qy	435	CAGCCCGCGGAAATTTCTCACAATAGTTTACAGGAACTGTCTCGGCTACAGTCAACAAAGA	494					
Db	1459	CAGCCCGCGGAAATTTCTCACAATAGTTTACAGGAACTGTCTCGGCTACAGTCAACAAAGA	1400					
Qy	495	CCCCGTCTCCAAAGGGTACTCACAGCAGTAGACAGGTGCGCTTCCCTGGTTCCG	554					
Db	1399	CCCCGTCTCCAAAGGGTACTCACAGCAGTAGACAGGTGCGCTTCCCTGGTTCCG	1340					
Qy	555	CGAGCTCCACACTCGATAGTATGTGGCTTCTTTACTGAGTATCTTTATTCGCTG	614					
Db	1339	CGAGCTCCACACTCGATAGTATGTGGCTTCTTTACTGAGTATCTTTATTCGCTG	1280					
Qy	615	GTGGGTTCTTTCGCTTCTCGATGTGCGCGGGCACAAATPACCACTTTCACCTTTGT	674					
Db	1279	GTGGGTTCTTTCGCTTCTCGATGTGCGCGGGCACAAATPACCACTTTCACCTTTGT	1220					
Qy	675	AAAGTCTGCTCTTTAGCAAAATTCGAAACCCCTTGGAGGTGAGGAGTTCCTACCTCTTC	734					
Db	1219	AAAGTCTGCTCTTTAGCAAAATTCGAAACCCCTTGGAGGTGAGGAGTTCCTACCTCTTC	1160					
Qy	735	CAAACTTCTCGGCACAAACAAATTAATCAAAAGGGAGATTGGAAAGCTCCCGTATTTT	794					
Db	1159	CAAACTTCTCTCCACAAACAAATTAATCAAAAGGGAGATTGGAAAGCTCCCGTATTTT	1100					
Qy	795	GTTTTTCTCTCTCGGAAGATTATTAAGGTGCAACACCCACCTCTTATGGGGTTCGGG	854					
Db	1099	GTTTTTCTCTCTCGGAAGATTATTAAGGTGCAACACCCACCTCTTATGGGGTTCGGG	1040					
Qy	855	GCCGCTTTTCTGCTTGCGCAATTTTCACTGACGCTGCCGAGGTGTCGCGCTGCCGAAGTG	914					

Db	1039	GCCTCTTTTCTGCTGGCAATTTTCACTGACGCTGCCGAGTGTCTGCGTGCAGAGTG	980						
Qy	915	CGCTGGTAACTACTACGACGCGCACTTCTTTCACTTTATAGATGACGATCAACAGGAG	974						
Db	979	CGCTGGTAACTACTACGACGCGCACTTCTTTCACTTTATAGATGACGTCGCGCAAGGAG	920						
Qy	975	GCCTTACCGCAGAGAAGACACCGCCCCCGCAGCCATCTTTGGCCAGATCTCCGCCCGG	1034						
Db	919	GCCTTACCGCAGAGAAGGACCGCCCCCGCAGCCATCTTTGGAAACATCTCTCCGGGAAG	860						
Qy	1035	CCCTGGCTCGTCCACCC-----CGCCACCGCTACCGTTGGAGAGGAAATATGCGAT	1088						
Db	859	ACCATATTTGGTACACCCCGCTTTCAGAAACCGTTACAGATGCGCGCGAAAGAGGATAT	800						
Qy	1089	CTTCAACACCGGCTCTCCCGCACTTTCGGATATACCTGTCAAGGCTACCAAGCTCAGAAC	1148						
Db	799	CTTCAATTTCCCGCTTTCTAGAGAAATTTGATCACCATATAAG---GAGGACACTCGCA	743						
Qy	1149	GCCTCTCTGGCGGTGGACATGATGAGATTTAATATTGACGACTTTTGTTCCTCCCGGAGG	1208						
Db	742	GCCATCTTGGAAATGTTAAACCACTCAGATTCAACATCGGCCAGTTCTCTCCCGCTCGG	683						
Qy	1209	GGGACCAACAAATCTCTATACCTTTTGAATCTACAGAAATAGAAAGGTTAAGTTGA	1268						
Db	682	CGGCACCAACCCCTTACCTTCCAAATCTACCGTATTAGAAAGGCTAAATATGA	623						
Qy	1269	ATTCTGGCCCTGCTCCCCATCACCCAGGTGATAGGGAGTGGGCTCCACTGCTGTAT	1328						
Db	622	ATTTTACCCAGAGACCCCATCACCTCTAATCAAGAGGTGTAGGTTCCACTGTTGTAT	563						
Qy	1329	TCTAGATGATAACTTTGTAAACAAAGGCCACAGCCCTTAACCTATGACCCATATGTAACTA	1388						
Db	562	CTTGGATGCCAACTTTGTAAACCCCTCCACCACTGGCTATGACCCCTATATACTA	503						
Qy	1389	CTCTCCCGCATAAATCCCTTCTCTACCACTCCGCTTACTCCGTTACTTCAACCCAA	1448						
Db	502	CTCTCCCGCCACACCAATAAGGCAACCTTTTACCTACCACTCCAGGTTACTTCAACCCCA	443						
Qy	1449	ACCTGTTCTTGTACTCCACCACTTGTATCTTCCAAACAAATAACAAAGGAATCAGCTTTG	1508						
Db	442	ACCTGAGCTGGACCAACAAATTTGTTGTTCCAGCCAAATAATAAAGAAACCAAGCTGTG	383						
Qy	1509	GATGAGGCTACAAACCTCTAGAAATGTGGACCACTAGGCTCGGCACTCGGTTTCAAAA	1568						
Db	382	GCTCCATTTAAATACCCACCAATATGTCGAGCACACAGGCTCGGCTTTCGGCTCCAAA	323						
Qy	1569	CAGTATATACGACGAGCTACAAATATCCGTGTAAACATGTATGTACAAATTCAGAGATT	1628						
Db	322	TGCAGACACAGCCCAAAATTTATGTGGTAAGGCTGACTATTTATGTACAAATTCAGAGA	263						
Qy	1629	TAATCTTAAAGACCCCACTTAAACCTTAAATGAATAAATAAATAAATAAATAAATAA	1688						
Db	262	TATCCTGAAAGACC-----CTCTAAATGAATAAATAAATAAATAAATAAATAA	214						
Qy	1689	GATAACAAAAAGACTCAGTAAATTTATTTTATATGGGAAAGGGCACAGGTTGGTCCAC	1748						
Db	213	GATAACAAAAAGACTCAGTAAATTTATTTTATATGGGAAAGGGCACAGGTTGGTCCAC	154						
Qy	1749	TGCTTCAAAATCGGCTTTCGGGTACC	1773						
Db	153	TGCTTCAAAATCGGCTTTCGGGTACC	129						

RESULT 10
ID ABX08220/c
ID ABX08220 standard; DNA; 1759 BP.
XX AC ABX08220;
XX AC
DT 20-JAN-2003 (first entry)
XX PK-15-Porcine circovirus (PK-15-PCV) genome.
XX DE
XX

Porcine circovirus genome; PCV; vaccine; type I PCV strain;
type II PCV strain; congenital tremor; pig; whole PCV vaccine;
passive immunisation; db.

Porcine circovirus.

W0200196377-A2.

20-DEC-2001.

15-JUN-2001; 2001WO-US019220.

15-JUN-2000; 2000US-0211710P.

(PURD) PURDUE RES FOUND.

Mittal SK, Stevenson GW, Choi J, Kiupel M, Kanitz CL;

WPI; 2002-106466/14.

N-FSDB; ABU02909, ABU02916, ABU02923, ABU02930, ABU02949, ABU02956.

New porcine circovirus (PCV) nucleic acids for use as a component of
vaccines for treating or preventing congenital tremors in pigs.

Example 1; Fig 1; 89pp; English.

The invention describes an isolated nucleic acid (I) from a porcine
circovirus (PCV) where (I) comprises a sequence coding for a circovirus
polypeptide. A vaccine comprising a PCV nucleic acid that encodes an
immunogenic polypeptide of type I or type II PCV strain and a carrier, is
useful for treating or preventing congenital tremors in a pig or its
progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II
is composed of PMS-PCV-P1, PMS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).
An isolated PCV strain (II) is useful for diagnosing a pathological cause
of congenital tremors in a pig which involves determining whether the pig
has been infected by PCV strain type I or type II. The determination of
the infection is effected by detecting the presence of a PCV nucleic acid
in a biological sample from the pig, by detecting hybridisation of an
oligonucleotide. Optionally, the determination of hybridisation is effected
by detecting the presence of PCV polypeptide in a biological sample from
the pig by detecting binding of an antibody that specifically binds a PCV
polypeptide. Optionally, the determination of infection is effected by
detecting the presence of antibodies directed against a PCV polypeptide
in a biological sample of the pig. An expression vector (III) encoding a
PCV polypeptide is useful as a vector vaccine against congenital tremors.
(II) along with a suitable adjuvant is useful as a whole PCV vaccine,
while the antigenic PCV polypeptides are used as components of subunit
vaccines. Antibodies against PCV proteins are useful in passive
immunisation strategies. This sequence represents a porcine circovirus
genome

Sequence 1759 BP; 432 A; 342 C; 510 G; 475 T; 0 U; 0 Other;

Query Match 68.3%; Score 1210.2; DB 6; Length 1759;

Best Local Similarity 84.9%; Pred. No. 0;

Matches 1397; Conservative 0; Mismatches 228; Indels 20; Gaps 3;

135 ACTGGGCGCCAAAAGGAAAGGACAGTACCCCTTTAGTCTCTCAGTCAATGATACCGGTC 194

1759 ACTGGGCGCCAAAAGGAAAGGACAGTACCCCTTTAGTCTCTCAGTCAATGATACCGGTC 1700

195 ACACAGTCTCAGTATGATCATCCCAAGGTAACAGCCATAAAAAATCATCCAAAAACAAC 254

1699 ACACAGTCTCAGTATGATCATCCCAAGGTAACAGCCATAAAAAATCATCCAAAAACAAC 1640

255 TTCTTCTCCATGATATCATCCACCACTTATTTCTACTAGGCTTCCAGTAGGTGTCCT 314

1639 TTCTTCTCCATGATATCATCCACCACTTATTTCTACTAGGCTTCCAGTAGGTGTCCT 1580

315 AGGCTCAGCAAAATTTACGGGCGCCACTGGCTCTCCCAACCGGGCGGCCACTATGAC 374

1579 AGGCTCAGCAAAATTTACGGGCGCCACTGGCTCTCTCCCAACCGGGCGGCCACTATGAC 1520

Qy 375 GTGTACAGCTGTCTTCCATACACGCTGTGTGATCTTCCCGCTCATTTCACAAAGTTTCAGC 434
Db 1519 GTGTACAGCTGTCTTCCATACACGCTGTGTGATCTTCCCGCTCATTTCACAAAGTTTCAGC 1460
Qy 435 CAGCCCGGGGAAATTTCTCACAATACGTTTACAGGAAACTGCTCGGCTCAGTCAACCAAGA 494
Db 1459 CAGCCCGGGGAAATTTCTCACAATACGTTTACAGGAAACTGCTCGGCTCAGTCAACCAAGA 1400
Qy 495 CCCCCTCTCCAAAAGGGTACTCAGCAGTATAGACAGTCTGCTGCGCTTCCCTGGTTCCG 554
Db 1399 CCCCCTCTCCAAAAGGGTACTCAGCAGTATAGACAGTCTGCTGCGCTTCCCTGGTTCCG 1340
Qy 555 CGGAGCTCCACATCGATAGTATGTGCTTCTTACTGAGTATTTCTTATTTCTGCTG 614
Db 1339 CGGAGCTCCACATCGATAGTATGTGCTTCTTACTGAGTATTTCTTATTTCTGCTG 1280
Qy 615 GTCGTTCTCTTTCGTTCTGATGTGCGGCGCACAAAATACCACTTTCACCTTGT 674
Db 1279 GTCGTTCTCTTTCGTTCTGATGTGCGGCGCACAAAATACCACTTTCACCTTGT 1220
Qy 675 AAAAGTCTGCTTTAGCAAAATTCGAAACCCCTGGAGGTGAGAGTTTACCTCTTC 734
Db 1219 AAAAGTCTGCTTTAGCAAAATTCGAAACCCCTGGAGGTGAGAGTTTACCTCTTC 1160
Qy 735 CAAACCTCTCTCGCACAAACAAATTAACAAAGGGAGATTGGAGCTCCCGTATTT 794
Db 1159 CAAACCTCTCTCGCACAAACAAATTAACAAAGGGAGATTGGAGCTCCCGTATTT 1100
Qy 795 GTTTTCTCTCTCGGAGGATTAATTAAGGTGAACACCCACCTCTTATGGGTTGCGG 854
Db 1099 GTTTTCTCTCTCGGAGGATTAATTAAGGTGAACACCCACCTCTTATGGGTTGCGG 1040
Qy 855 GCCCTTTCTTGTCTGGCAATTTTCACTGACGCTGCCGAGGTGCTGCGCTGCCGAAGTG 914
Db 1039 GCCCTTTCTTGTCTGGCAATTTTCACTGACGCTGCCGAGGTGCTGCGCTGCCGAAGTG 980
Qy 915 CGCTGGTAATTAACAGCAGGCGCACTTCTTCACTTTTATAGGATGAGTATCAAGAG 974
Db 979 CGCTGGTAATTAACAGCAGGCGCACTTCTTCACTTTTATAGGATGAGTATCAAGAG 920
Qy 975 CGCTTACCGGAGAGAGACACCGCCCGCAGGCATCTTGGCCAGATCTCCGCGCGCG 1034
Db 919 CGCTTACCGGAGAGAGAGACCGCCCGCAGGCATCTTGGAAACATCTTCCGGAGAG 860
Qy 1035 CCCCCTGCTCGTCCACCC-----CCGCCACCGCTACCGTTGGAGAGGAAATTTGGAT 1088
Db 859 ACCATATTTGGCACACCGCCCTTTCAGAAACGTTTACAGATGGCGCCGAAAGCGGTAT 800
Qy 1089 CTTCAACACCGCGCTCTCCCGCACCTTCGGATATATCTGTCAAGGCTACCAGTCAAGAC 1148
Db 799 CTTCAATTTCCGCGCTTTCTACAGAAATTTGTACTCACCATAAAG---GAGGATACTCGCA 743
Qy 1149 GCCCTCTGGGCGGTGACATGATGAGATTTAATTTAGCAGCTTTGTTCCTCCCGGAGG 1208
Db 742 GCCATTTGGATGTTTAACTTACCTCAATTTCAATTCGGCAGTTCCTCCCGCTCAGG 683
Qy 1209 GGGGACCAACAAATCTCTATACCTTTTGAATACTACAGATAAGAAAGGTTAAGTTGA 1268
Db 682 CGGCACCAACCCCTACCCCTACCTTTTCAATCTACCGCTATTAGAAGGCTTAATATGA 623
Qy 1269 ATTCTGGCGCTCTCCCGCATACCCAGGGTGATAGGGGAGTGGGCTCCTACTGTGTTAT 1328
Db 622 ATTTTACCCAGAGACCCCATCACCTCTAATCAAGAGGTGTTGGGCTCCTACTGTGTTAT 563
Qy 1329 TCTAGATGATTAATTTGTAAAGGGCCAGCCCTAACCTATACCCCATATGATAACTA 1388
Db 562 CTTGGATGCCAATTTGTAAACCCCTCCACCACTTGGCTTATGACCCCTATATTAATA 503
Qy 1389 CTCCTCCCGGCATACAAATCCCGCCCAACCTTCTCTCACTCCCTCCGCTTACTTACACCCAA 1448
Db 502 CTCCTCCCGGCACCAATAGGAGAGCCCTTTACCTCACTCCAGGTACTTCAACCCCAA 443
Qy 1449 ACCTGTTCTTGACTCCACCATTTGATTAATCTTCCAAACCAAAATAAAGGAATCAGTTTG 1508

QY 895 GTGCTGCGCTGCGCGAGTGGCTGGTAATCTACAGAGCGCACTTCTTCACTTTAT 954
 Db |||||
 QY 665 GTGCTGCGCTGCGCGAGTGGCTGGTAATCTACAGAGCGCACTTCTTCACTTTAT 606
 Db |||||
 QY 955 AGGATGACGTATCCCAAGGAGGCTTACCGCAGAGACACCGCCCGCAGCCATCTT 1014
 Db |||||
 QY 605 AGGATGACGTGCGCAAGGAGGCTTACCGCAGAGAGACCGCCCGCAGCCATCTT 546
 Db |||||
 QY 1015 GCGCAGATCTCTCGCGCGCGCCCTGGCTCGTCCACCC-----CGGCCACCGCTACCGT 1068
 Db |||||
 QY 545 GGAATACCTCTCGCAGAGACCATATTTGGCAGACCGCCGCTTCAGAAACGGTACAGA 486
 Db |||||
 QY 1069 TGGAGAGAGAAATGGCATCTTCAACACCGCCCTCTCCGACACCTTCGGATATCTGTC 1128
 Db |||||
 QY 485 TGGCGCCGAAAGACGGGTATCTTCAATTTGCCGCTTCTAGAGAATTTGTACTCAC---C 429
 Db |||||
 QY 1129 AAGGCTACACAGTCAGAACGCCCTCTCGGGGGTGGACATGATCAGATTTAATTCAC 1188
 Db |||||
 QY 428 ATAGAGAGGACACTCGGAGGCATCTTGGAAATGTTAACAGCTCAGATTCACATCGGC 369
 Db |||||
 QY 1189 GACTTTGTTCCCGCGGAGGGGACCAACAAATCTCTATACCTTTTGAATACTACAGA 1248
 Db |||||
 QY 368 CAGTTCTCTCCCGCTCAGGGGGCACCACCCCTACCTTCTCCATACTACCGT 309
 Db |||||
 QY 1249 ATAGAAAGGTTAAGTTGAATCTGGCGCTGCTCCCGATCACCAGGGTGATGGGA 1308
 Db |||||
 QY 308 ATTAGAAAGGCTAAATATGAAATTTTACCCGAGAGACCCCATCACCTCTAATCAAGAGGT 249
 Db |||||
 QY 1309 GTGGCTCCACTGCTGTTATTCTAGATGATACTTTGTAACAAAGGCCACAGCCCTAAC 1368
 Db |||||
 QY 248 GTTGGTCCACTGCTGTTATCTTGGATGCCAACTTTGTAACCCCTCCACCACTTGCC 189
 Db |||||
 QY 1369 TATGACCATATGTAATCTCTCCCGCCATACAATCCCGCAACCTTCTCTTACCAC 1428
 Db |||||
 QY 188 TATGACCTATATTAATCTCTCTCCCGCCACACATTAAGCGCTTTTACCTTACCAC 129
 Db |||||
 QY 1429 TCCGTTACTTACACCAACCTGTTCTTGATCCACATGATTAATCTTCAACCAAT 1488
 Db |||||
 QY 128 TCCAGGTACTTACCCCCCAACCTGAGCTGGACCAACAATTTGATTTGCTCAGCCAA 69
 Db |||||
 QY 1489 AACAAAGGAATCAGCTTTGGATGAGGCTACAACTCTAGAAATGTGGACCACTAGGC 1548
 Db |||||
 QY 68 ANTAAGAAACCACTGTGGCTCCATTTAATATCCACCAATGTGCAACACAGGC 9
 Db |||||
 QY 1549 CTCG 1552
 Db |||||
 8 CTAG 5

RESULT 12

ABX94361/c
 ID ABX94361 standard; DNA; 7460 BP.

XX AC ABX94361;

XX DT 19-JUN-2003 (first entry)

XX DE Rolling circle replicon construct pCI-CVI-luc.

XX KW Virucide; vaccine; gene therapy; Rep gene; rolling circle replication;

XX KW pCI-CVI-luc; PCV; ds; luciferase.

XX OS Porcine circovirus.

XX OS Photinus pyralis.

XX OS Synthetic.

XX XX US2002187952-A1.

XX XX 12-DEC-2002.

XX XX 20-DEC-2001; 2001US-00038001.

XX XX 16-FEB-2000; 2000US-00505477.

XX XX

XX XX

XX (PALM/) PALMER K E.
 PA (POGU/) POGUE G G.
 PA (MCCO/) MCCORMICK A.

XX Palmer KE, Pogue GG, McCormick A;

XX WPI; 2003-341042/32.

XX New rolling circle DNA replicons or polynucleotides, useful in vaccine or
 PT gene therapy applications, for eliciting an immunization reaction in a
 PT eukaryotic host, or for inducing or enhancing a function or trait in a
 PT host eukaryotic cell.

XX Example 2; Fig 8; Sipp; English.

XX The invention relates to a polynucleotide capable of eliciting an
 CC immunisation reaction in a eukaryotic host to a peptide or polypeptide.
 CC The polynucleotide encodes the peptide or polypeptide, and contains
 CC elements of a viral genome (i.e. the Rep gene) that is capable of rolling
 CC circle replication. The peptide or polypeptide is capable of expression
 CC in the eukaryotic host. Also included are constructing a polynucleotide
 CC capable of eliciting an immunisation reaction in a host (comprising
 CC inserting a sequence encoding a peptide or polypeptide into the
 CC polynucleotide, where the polynucleotide comprises elements of a viral
 CC genome that is capable of rolling circle replication) and immunising a
 CC host comprising administering a composition comprising the polynucleotide
 CC into the host. Substantially higher levels of IgG antibody induction were
 CC seen in mice injected with immunogenic protein insert linked to a rolling
 CC circle replication cassette versus immunogenic protein inserted into a
 CC non-rolling circle replicon mammalian expression vector. Levels of IgG
 CC antibody through successive bleeds were higher for both luciferase and
 CC beta-galactosidase expression cassettes linked to a porcine Circovirus
 CC cassette, as compared to non-rolling circle replicon linked vectors or
 CC injection with saline alone, vector without insert, purified luciferase
 CC or beta-galactosidase. The polynucleotide capable of rolling circle
 CC replication in a eukaryotic host is useful in vaccine or gene therapy
 CC applications, or for eliciting an immunisation reaction in a eukaryotic
 CC host. The rolling circle replicons or polynucleotides are also useful for
 CC the discovery of the function of genes in eukaryotic hosts, or for inducing
 CC or enhancing a function or trait in a host eukaryotic cell, or for down-
 CC regulating a gene in a plant or mammalian cells, which alters or even
 CC eliminates the function of that gene. The ancillary protein is useful for
 CC potentiating an immunisation reaction in the host elicited by the peptide
 CC or polypeptide. The present sequence (termed pCI-CVI-luc) is a
 CC polynucleotide of the invention comprising the whole PCV (porcine
 CC circovirus) cloned into a vector containing a luciferase reporter gene

XX Sequence 7460 BP; 1911 A; 1676 C; 1897 G; 1986 T; 0 U; 0 Other;

XX Query Match 67.5%; Score 1196.8; DB 8; Length 7460;
 XX Best Local Similarity 86.8%; Pred. No. 0;
 XX Matches 1357; Conservative 0; Mismatches 192; Indels 15; Gaps 3;

QY 1 GGTACCTCCGTGGATTGTTCTCCAGCAGCTTCCAAAATTCGAAAGTAGTAGTCTCCGA 60
 Db 1565 GGTACCTCCGTGGATTGTTCTCCAGCAGCTTCCAAAATTCGAAAGTAGTAGTCTCCGA 1506

QY 61 TAGAGAGCTTCTACAGCTGGGACAGCAGTTCAGAGGTACCATTCCTGGGGGCGCTGATTG 120
 Db 1505 TAGAGAGCTTCTACAGCTGGGACAGCAGTTCAGAGGTACCATTCCTGGGGGCGCTGATTG 1446

QY 121 CTGTAATCAAAATACCTGCGGGCCAAAAGAGAACAGTACCCCTTTAGTCTCTACAGTC 180
 Db 1445 CTGTAATCAAAATACCTGCGGGCCAAAAGAGAACAGTACCCCTTTAGTCTCTACAGTC 1386

QY 181 AATGGATACCGGTACACAGTCTCAGTAGATCATCCAGGTAAACGCCATAAAATCA 240
 Db 1385 AATGGATACCGGTACACAGTCTCAGTAGATCATCCAGGTAAACGCCATAAAATCA 1326

QY 241 TCCAAAACCAACTTCTTCTCCATGATATCCATCCCAACCACTTATTTCTACTAGGCTTC 300
 Db 1325 TCCAAAACCAACTTCTTCTCCATGATATCCATCCCAACCACTTATTTCTACTAGGCTTC 1266

Qy 301 CAGTAGGTGTCCTAGGCTCAGCAAAATTAAGGCGCCCACTGGCTCTTCCACCAACCGGGC 360
 Db |||||
 Qy 1265 CAGTAGGTGTCCTAGGCTCAGCAAAATTAAGGCGCCCACTGGCTCTTCCACCAACCGGGC 1206
 Db |||||
 Qy 361 GGGCCCACTATGAGCTGTACAGCTGTCTTCAATACAGCTGTCTGCAATCTTCCCGCTCACT 420
 Db |||||
 Qy 1205 GGGCCCACTATGAGCTGTACAGCTGTCTTCAATACAGCTGTCTGCAATCTTCCCGCTCACT 1146
 Db |||||
 Qy 421 TTCAAAAGTTGAGCGCCCGCGGAAATTTCTACATACGTTACAGCAAACTGCTCGGCT 480
 Db |||||
 Qy 1145 TTCAAAAGTTGAGCGCCCGCGGAAATTTCTACATACGTTACAGCAAACTGCTCGGCT 1086
 Db |||||
 Qy 481 ACAGTACCAAAAGACCCGCTCTCCAAAAGGTAATCTACAGCAGTAGACAGTGTCTGCGC 540
 Db |||||
 Qy 1085 ACAGTACCAAAAGACCCGCTCTCCAAAAGGTAATCTACAGCAGTAGACAGTGTCTGCGC 1026
 Db |||||
 Qy 541 TTCCCTCGGTTCCGCGAGCTCCACACTCGAATAGTAGTGCGCTCTTTTA-----CTG 594
 Db |||||
 Qy 1025 TTCCCTCGGTTCCGCGAGCTCCACACTCGAATAGTAGTGCGCTCTTTTACTGCGAGCTG 966
 Db |||||
 Qy 595 CAGTATTTCTTATCTGCTGGTGGTTCCTTTCGCTTCTCGATGTCGAGCGGGCACCA 654
 Db |||||
 Qy 965 CAGTATTTCTTATCTGCTGGTGGTTCCTTTCGCTTCTCGATGTCGAGCGGGCACCA 906
 Db |||||
 Qy 655 AAATACCACCTTCACTTTGTTAAAGTCTGCTTCTTAGCAAAATTCGCAAAACCCCTGGAGG 714
 Db |||||
 Qy 905 AAATACCACCTTCACTTTGTTAAAGTCTGCTTCTTAGCAAAATTCGCAAAACCCCTGGAGG 846
 Db |||||
 Qy 715 TGAGGAGTTTACCCCTTTCACAACTTCTCGGCCACAAACAAATTAATCAAAAGGGAG 774
 Db |||||
 Qy 845 TGAGGAGTTTACCCCTTTCACAACTTCTCGGCCACAAACAAATTAATCAAAAGGGAG 786
 Db |||||
 Qy 775 ATTGGAAGCTCCGTAATTTGTTTCTTCTCTCGGAAGGATTAATGAAGGTGAACACC 834
 Db |||||
 Qy 785 ATTGGAAGCTCCGTAATTTGTTTCTTCTCTCGGAAGGATTAATGAAGGTGAACACC 726
 Db |||||
 Qy 835 CACCTCTTATGGGGTTCGGGCGCTTCTTCTGCTGGCATTTTCACTGACGCTGCCGAG 894
 Db |||||
 Qy 725 CACCTCTTATGGGGTTCGGGCGCTTCTTCTGCTGGCATTTTCACTGACGCTGCCGAG 666
 Db |||||
 Qy 895 GTGTCGCGCTGCCGAGTGGCTGTTAATCTACAGCAGCGCATTTCTTTCACTTTAT 954
 Db |||||
 Qy 665 GTGTCGCGCTGCCGAGTGGCTGTTAATCTACAGCAGCGCATTTCTTTCACTTTAT 606
 Db |||||
 Qy 955 AGATGAGCTATCAAGGAGCGTTACGGCAGAGAGACACCGCCCGCGAGCCATCTT 1014
 Db |||||
 Qy 605 AGATGAGCTATCAAGGAGCGTTACGGCAGAGAGAGACCGCCCGCGAGCCATCTT 546
 Db |||||
 Qy 1015 GGCCAGATCTCCGCGCGCCCTGCTGCTGCCACCC-----CCGCCACCGCTACCGT 1068
 Db |||||
 Qy 545 GGAACATCTCCGCAAGACCATATTTGGCACACCCCGCTTCAGAAACCGTTACAGA 486
 Db |||||
 Qy 1069 TGGAGAGGAAATAGGATCTTCAACACCGCTCTCCGCGCATCTTCGGATATCTGTC 1128
 Db |||||
 Qy 485 TGGCGCGAAAGACGGGTATCTTCAATTCGCGCTCTTACAGAAATTTGTAATCTAC 429
 Db |||||
 Qy 1129 AAGCTACCAAGTACAGACCGCTCTGCGGCTGGACATGATGAGATTAATATTGAC 1188
 Db |||||
 Qy 428 ATAGAAGGAGACACTCGAGCCATCTTGGAAATGTTAACACGCTCAGATTCACATCGGC 369
 Db |||||
 Qy 1189 GACTTTGTTCCCGGAGGGGGGACCAACAAATCTCTATACCCTTTTGAATCTACAGA 1248
 Db |||||
 Qy 368 CAGTTCTCCCTCCCTCAGGCGGACCAACCCCTACCTTCCCTTCCATCTACCGT 309
 Db |||||
 Qy 1249 ATAGAAGGTTAAGGTTGAATTCGCGCTGCTCCCGCATCACCGAGGTGATAGGGGA 1308
 Db |||||
 Qy 308 ATAGAAGGTTAAGGTTGAATTTTACCCAGAGACCCCATCTCAATCAAAAGGT 249
 Db |||||
 Qy 1309 GTGGGCTCCACTGCTGTATTTCTAGATGATTAATTTGTAAAGGGCCACAGCCCTTACC 1368
 Db |||||
 Qy 248 GTTGGGCTCCACTGCTGTATTTCTGGATGCCAACTTTGTAAACCCCTCCACCACTTGCC 189
 Db |||||

Qy 1369 TATGACCCATATGTAATACTACTCTCCCGCCATACAAATCCCAAGCCCTTCTCTACCAC 1428
 Db |||||
 Qy 188 TATGACCCCTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 129
 Db |||||
 Qy 1429 TCCGTTTACTTACACCCCAACCTTCTTGACTCCACCAATTTGATTTACTTCCCAACCAAT 1488
 Db |||||
 Qy 128 TCAGGTACTTCCACCCCAACCTGAGCTGGACCAATTTGATTTGGTTCCAGCCAAAT 69
 Db |||||
 Qy 1489 AACAAAGGAATCAGCTTTGGATGAGGCTACAAACCTCTAGAAATGAGACCACTGATAGC 1548
 Db |||||
 Qy 68 AATAAAGAAACCAAGCTGTGGCTCCATTTAAATACCCACCAATGTCGACCAACAGGC 9
 Db |||||
 Qy 1549 CTCG 1552
 Db |||||
 Qy 8 CTAG 5

RESULT 13
 AAH74865/c
 ID AAH74865 standard; DNA; 5285 BP.
 XX
 AC AAH74865;
 XX
 DT 29-OCT-2001 (first entry)
 XX
 DE Nucleotide sequence of a construct comprising the PCV Rep gene.
 XX
 KW Rolling circle replication; RCR; Rep gene; gene function; Geminivirus;
 KW Circovirus; Nanovirus; gene therapy; PCV; ss.
 XX
 OS Synthetic.
 OS Porcine circovirus.
 XX
 PN W0200161024-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 15-FEB-2001; 2001WO-US005394.
 XX
 PR 16-FEB-2000; 2000US-00505477.
 XX
 PA (LARG-) LARGE SCALE BIOLOGY CORP.
 XX
 PI Palmer KE, Pogue GP;
 XX
 PS WPI; 2001-522601/57.
 XX
 XX New polynucleotide capable of rolling circle replication in host, useful for discovery of gene function, comprises Rep gene, sequences that are cis on the polynucleotide and open reading frame encoding protein of interest.
 PT
 PT
 PT
 PT
 PS
 XX
 XX
 CC The specification describes a polynucleotide that is capable of rolling circle replication (RCR) in an eukaryotic host. The polynucleotide comprises a Rep gene encoding from a virus, sequences that are cis on the polynucleotide such that the Rep protein can bring about RCR of the polynucleotide, an open reading frame encoding a protein of interest capable of being expressed in the host, and optionally a multiple cloning site, where the polynucleotide lacks genes of the virus. The virus is selected from the group of genera of family Geminiviridae, Circoviridae and Nanovirus. The polynucleotide sequence is useful for the discovery of the function of genes in eukaryotic hosts, and for inducing or enhancing a trait in a host eukaryotic cell, for down-regulating a gene in a plant or in mammalian cell and thus altering or even eliminating the function of that gene, as gene sequence delivery tools for mammalian genomic approaches, for gene therapy applications (for delivering therapeutic or complementing gene products to organisms or cells), and in whole animal genomics. The present sequence represents a construct comprising the whole PCV genome. This construct contains the PCV Rep gene under the transcriptional control of its own promoter, and has the putative coat protein inactivated by insertion of the bacterial cloning vector

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XX SQ Sequence 5285 BP; 1216 A; 1277 C; 1514 G; 1278 T; 0 U; 0 Other;
Query Match 67.4%; Score 1195.8; DB 4; Length 5285;
Beat Local Similarity 87.7%; Pred. No. 0;
Matches 1331; Conservative 0; Mismatches 177; Indels 9; Gaps 2;

Qy 1 GGTACTCCGTGGATGTTCTCCAGCAGTCTTCCAAAATTGCAAAAGTAGTAAATCCTCCGA 60
Db GGTACTCCGTGGATGTTCTCCAGCAGTCTTCCAAAATTGCAAAAGTAGTAAATCCTCCGA 1801

Qy 61 TAGAGAGCTTTACAGCTGGGACAGCAGTGGAGGTACCATTCCTGGGGGGCCTGATTG 120
Db TAGAGAGCTTTACAGCTGGGACAGCAGTGGAGGTACCATTCCTGGGGGGCCTGATTG 1741

Qy 121 CTGGTAATCAAAATCTCGGGCCAAAAGAACAGTAGTACCCCTTTTAGTCTCTACAGTC 180
Db CTGGTAATCAAAATCTCGGGCCAAAAGAACAGTAGTACCCCTTTTAGTCTCTACAGTC 1681

Qy 1740 CTGGTAATCAAAATCTCGGGCCAAAAGAACAGTAGTACCCCTTTTAGTCTCTACAGTC 1681
Db CTGGTAATCAAAATCTCGGGCCAAAAGAACAGTAGTACCCCTTTTAGTCTCTACAGTC 1681

Qy 181 AATGATACCGGTTCACAGTCTCAGTAGATCATCCCAAGGTAAACGCCATAAAATCA 240
Db AATGATACCGGTTCACAGTCTCAGTAGATCATCCCAAGGTAAACGCCATAAAATCA 1621

Qy 241 TCCAAAACAAACTTCTTCCATGATATCCATCCCACTTATTTCTACTAGGCTTC 300
Db TCCAAAACAAACTTCTTCCATGATATCCATCCCACTTATTTCTACTAGGCTTC 1561

Qy 301 CAGTAGGTGTCCTAGGCTCAGCAAAATTAAGGGCCCACTGGCTCTTCCCAACACCGGGC 360
Db CAGTAGGTGTCCTAGGCTCAGCAAAATTAAGGGCCCACTGGCTCTTCCCAACACCGGGC 1501

Qy 361 GGGCCCACTAAGCTGTACAGTGTCTTCCAATCAAGCTGTGCAATCTTCCCGTCACT 420
Db GGGCCCACTAAGCTGTACAGTGTCTTCCAATCAAGCTGTGCAATCTTCCCGTCACT 1441

Qy 421 TTCAAAAGTTCAGCCAGCCGGGAAATTTCTCAGATAGTTTACAGGAACTGCTCGGCT 480
Db TTCAAAAGTTCAGCCAGCCGGGAAATTTCTCAGATAGTTTACAGGAACTGCTCGGCT 1381

Qy 481 ACAGTCACAAAGACCCCGTCTCCAAAAGGTACTCACAGAGTAGACAGCTGCTGGCG 540
Db ACAGTCACAAAGACCCCGTCTCCAAAAGGTACTCACAGAGTAGACAGCTGCTGGCG 1321

Qy 541 TTCCCTCGGTTCCGGAGCTCCACATCGATAGTATGTGGCTTTCTTTACTGCAAT 600
Db TTCCCTCGGTTCCGGAGCTCCACATCGATAGTATGTGGCTTTCTTTACTGCAAT 1261

Qy 601 TCTTTATTTCTGCTGCTGCTGCTTCTTCTGCTTCTGATGTGGCAGCGGACCAAAATAC 660
Db TCTTTATTTCTGCTGCTGCTGCTTCTTCTGCTTCTGATGTGGCAGCGGACCAAAATAC 1201

Qy 661 CACTTCACCTTGTAAAAGTCTGCTTCTTAGCAAAATTCGAAACCCCTGGAGGTGAGGA 720
Db CACTTCACCTTGTAAAAGTCTGCTTCTTAGCAAAATTCGAAACCCCTGGAGGTGAGGA 1141

Qy 721 GTTCTACCTCTTCCAAACCTTCTCGCCCAAAACAAATTAATCAAAAGGGAGATTGGA 780
Db GTTCTACCTCTTCCAAACCTTCTCTCTCGCAAAACAAATTAATCAAAAGGGAGATTGGA 1081

Qy 781 AGCTCCCGTATTTGTTTTCTCTCTCGGAGGATTAATTAAGGGTGAACACCCACCTC 840
Db AGCTCCCGTATTTGTTTTCTCTCTCGGAGGATTAATTAAGGGTGAACACCCACCTC 1021

Qy 841 TTATGGGTTGCGGCGCTTTTCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTG 900
Db TTATGGGTTGCGGCGCTTTTCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTG 961

Qy 901 CCGCTGCCGAAGTGGCTGGTAATACTACAGCAGCAGCTCTTTTCACTTTTATAGGATG 960
Db CCGCTGCCGAAGTGGCTGGTAATACTACAGCAGCAGCTCTTTTCACTTTTATAGGATG 901

Qy 961 ACGTATCCAGAGGCGTTACCGCAAGAGAGACACCGCCCGCGAGCCATCTTGGCCAG 1020
Db ACGTATCCAGAGGCGTTACCGCAAGAGAGAGACACCGCCCGCGAGCCATCTTGGCCAG 1020
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Db 900 ACGTGGCCAGAGGCGGTTACCGCAGAGAGAGGACCCCGCCCGCAGCCATCTTGGAAAC 841
Qy 1021 ATCTCCGCCCGCCCGCTGCTGCTCCACCC-----CCGCCACCGCTACCGTTGGAGA 1074
Db 840 ATCTCCCGGAGAGACCATATTTGGCACACCCCGCTTTCAGAAACCGTTACAGATGGCG 781
Qy 1075 AGGAAAATGCGATCTTCAACACCGGCTCTCCCGCAGCTTCGGGATATCTGTCAAGCT 1134
Db 780 CGAAAGACGGGTATCTTCAATTCGCGCTTTCTACAGAAATTTGTACTCACCATAAAGGA 721
Qy 1135 ACCACAGTCAGAACGCGCTCTGCGGCGTGACATGATGAGATTTAAATATTGACGACTTT 1194
Db 720 G---GATACTCGAGCCACTTTGGAATGTTAACTTACCTCAAAATTCACATCGGCCAGTTC 664
Qy 1195 GTTCCCCCGGAGGGGGACCAACAAAATCTCTATACCTTTTGAATACTACAGATAAGA 1254
Db 663 CTCCCCCTCAGGGGCGACCAACCCCTACCTTCCCTTTTCCAATACTACCGTATTAGA 604
Qy 1255 AAGGTTAAGGTTGAATTTCTGCGCTCTGCTCCCGCATACCCAGGGTGATAGGGAGTGGC 1314
Db 603 AAGGCTAAATATGAATTTTACCCAGAGACCCCATCACCTCTAATCAAGAGGTGTTGGG 544
Qy 1315 TCCACTGCTGTTATTCTAGATGATAAATTTTGTAAAGGCGCACAGCCCTAACCTPATGAC 1374
Db 543 TCCACTGTTGTTATCTGGATGCCAATTTTGTAAACCCCTCACCACTTGGCCTPATGAC 484
Qy 1375 CCATATGTAAACTACTCTCTCCCGCCATACAAATCCCCCAACCCCTTCTCTACCACTCCCGT 1434
Db 483 CCCTATATTAACTACTCTCTCCCGCCACACCATTAAGGAGCCCTTTTACCTACCACTCCAGG 424
Qy 1435 TACTTTCACACCAAACTGTTCTTGTGATCTTCAACCATTAATCTTCCAAACCAATAACAA 1494
Db 423 TACTTTCACCCCAAACTGAGCTGGACCAAAATTTGATTTGTTTCCACCCCAATAATAA 364
Qy 1495 AGGAATCAGCTTTGGAT 1511
Db 363 AGAAACCGAGCTGTGGCT 347

RESULT 14
ABX94355/C
ID ABX94355 standard; DNA; 5285 BP.
XX
AC ABX94355;
XX
DT 19-JUN-2003 (first entry)
XX
DE Rolling circle replicon construct 1.
XX
KW Virucide; vaccine; gene therapy; Rep gene; rolling circle replication;
KW Construct 1; PCV; ds.
XX
OS Porcine circovirus.
OS Simian virus 40.
OS Synthetic.
XX
FN US2002187952-A1.
XX
PD 12-DEC-2002.
XX
PF 20-DEC-2001; 2001US-00038001.
XX
PR 16-FEB-2000; 2000US-00505477.
XX
PA (PALM/) PALMER K E.
PA (POGU/) POGUE G G.
PA (MCCO/) MCCORMICK A.
XX
PI Palmer KE, Pogue GG, McCormick A;
XX
DR WPI; 2003-341042/32.
XX
PT New rolling circle DNA replicons or polynucleotides, useful in vaccine or
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gene therapy applications, for eliciting an immunization reaction in a eukaryotic host, or for inducing or enhancing a function or trait in a host eukaryotic cell.

Example 1; Fig 5; S1pp; English.

The invention relates to a polynucleotide capable of eliciting an immunisation reaction in a eukaryotic host to a peptide or polypeptide. The polynucleotide encodes the peptide or polypeptide, and contains elements of a viral genome (i.e. the Rep gene) that is capable of rolling circle replication. The peptide or polypeptide is capable of expression in the eukaryotic host. Also included are constructing a polynucleotide capable of eliciting an immunisation reaction in a host (comprising inserting a sequence encoding a peptide or polypeptide into the polynucleotide, where the polynucleotide comprises elements of a viral genome that is capable of rolling circle replication) and immunising a host comprising administering a composition comprising the polynucleotide into the host. Substantially higher levels of Igg antibody induction were seen in mice injected with immunogenic protein insert linked to a rolling circle replication cassette versus immunogenic protein inserted into a non-rolling circle replicon mammalian expression vector. Levels of Igg antibody through successive bleeds were higher for both luciferase and beta-galactosidase expression cassettes linked to a porcine Circovirus cassette, as compared to non-rolling circle replicon linked vectors or injection with saline alone, vector without insert, purified luciferase or beta-galactosidase. The polynucleotide capable of rolling circle replication in a eukaryotic host is useful in vaccine or gene therapy applications, or for eliciting an immunisation reaction in a eukaryotic host. The rolling circle replicons or polynucleotides are also useful for the discovery of the function of genes in eukaryotic hosts, for inducing or enhancing a function or trait in a host eukaryotic cell, or for down-regulating a gene in a plant or mammalian cells, which alters or even eliminates the function of that gene. The ancillary protein is useful for potentiating an immunisation reaction in the host elicited by the peptide or polypeptide. The present sequence (termed Construct 1) is a polynucleotide of the invention comprising the whole pCV (porcine circovirus) cloned into the Invitrogen cloning vector pCR BLUNT II-TOPO. The pCV Rep gene is under control of its own promoter and the coat protein gene is inactivated by insertion of the vector

Sequence 5285 BP; 1216 A; 1276 C; 1515 G; 1278 T; 0 U; 0 Other;
 Query Match 67.4%; Score 1195.8; DB 8; Length 5285;
 Best Local Similarity 87.7%; Pred. No. 0;
 Matches 1331; Conservative 0; Mismatches 177; Indels 9; Gaps 2;
 1 GGTACCTCCGTTGATTGTTCTCCAGCAGTCTTCCAAAATTCGAAAGTAGTAATCCTCCGA 60
 1860 GGTACCTCCGTTGATTGTTCTCCAGCAGTCTTCCAAAATTCGAAAGTAGTAATCCTCCGA 1801
 61 TAGAGAGCTTCTACAGCTGGACAGCAGTTGAGAGTACCATTCCTCGGGGGCTGATTG 120
 1800 TAGAGAGCTTCTACAGCTGGACAGCAGTTGAGAGTACCATTCCTCGGGGGCTGATTG 1741
 121 CTGGTAATCAAAATACCTGCGGGCCAAAAGGAACAGTACCCCTTTAGTCTCTACAGTC 180
 1740 CTGGTAATCAAAATACCTGCGGGCCAAAAGGAACAGTACCCCTTTAGTCTCTACAGTC 1681
 181 AATGGATACCGGTACACAGTCTCAGTAGATCATCCCAAGTAAACAGCCATAAAATCA 240
 1680 AATGGATACCGGTACACAGTCTCAGTAGATCATCCCAAGTAAACAGCCATAAAATCA 1621
 241 TCCAAAACAACTTCTTCCATGATATCCATCCACCACTTATTTCTACTAGGCTTC 300
 1620 TCCAAAACAACTTCTTCCATGATATCCATCCACCACTTATTTCTACTAGGCTTC 1561
 301 CAGTAGGTGTCCTTAGGCTCAGCAAAATTAAGGGCCCACTGGCTCTTCCACACACCGGGC 360
 1560 CAGTAGGTGTCCTTAGGCTCAGCAAAATTAAGGGCCCACTGGCTCTTCCACACACCGGGC 1501
 361 GGGCCCACTATGACGTGTACAGTGTCTTCCATACAGCTGTGTCATCTTCCCGCTCACT 420
 1500 GGGCCCACTATGACGTGTACAGTGTCTTCCATACAGCTGTGTCATCTTCCCGCTCACT 1441

Qy 421 TTCAAAGTTTCAGCCAGCCGCGGAAATTTCTCACATACGTTTACAGGAACTGCTCGGCT 480
 Db 1440 TTCAAAGTTTCAGCCAGCCGCGGAAATTTCTCACATACGTTTACAGGAACTGCTCGGCT 1381
 Qy 481 ACAGTCACCAAGACCCCGCTCTCCAAAAGGGTACTCACAGCAGTAGACAGTTCGCTGCGC 540
 Db 1380 ACAGTCACCAAGACCCCGCTCTCCAAAAGGGTACTCACAGCAGTAGACAGTTCGCTGCGC 1321
 Qy 541 TTCCCTCGTTTCGCGGAGCTCACACTCGATAAGTATGCGGCTTCTTTTACTGCAATAT 600
 Db 1320 TTCCCTCGTTTCGCGGAGCTCACACTCGATAAGTATGCGGCTTCTTTTACTGCAATAT 1261
 Qy 601 TCTTTATCTGCTGCTGCTGCTTCTTCTCGATGCGGAGCGGGGACCAAAATATAC 660
 Db 1260 TCTTTATCTGCTGCTGCTGCTTCTTCTCGATGCGGAGCGGGGACCAAAATATAC 1201
 Qy 661 CACTTCACCTTGTAAAGTCTGCTTCTTTAGCAAAATTCGCAAAACCCCTCGAGGTAGGA 720
 Db 1200 CACTTCACCTTGTAAAGTCTGCTTCTTTAGCAAAATTCGCAAAACCCCTCGAGGTAGGA 1141
 Qy 721 GTTCTACCTTCTCCAAAACCTTCTCGCCACCAAAATAATCAAAAAGGAGATGGA 780
 Db 1140 GTTCTACCTTCTCCAAAACCTTCTCGCCACCAAAATAATCAAAAAGGAGATGGA 1081
 Qy 781 AGCTCCGCTATTTGTTTCTCTCTCTCGAAAGGATTAATAAGGGTGAACACCCACTC 840
 Db 1080 AGCTCCGCTATTTGTTTCTCTCTCGAAAGGATTAATAAGGGTGAACACCCACTC 1021
 Qy 841 TTATGGGTTGCGGGCGCTTTTCTGCTTGGCATTTTCTACTCACTGCTGCGAGGTGCTG 900
 Db 1020 TTATGGGTTGCGGGCGCTTTTCTGCTTGGCATTTTCTACTGACGCTGCGAGGTGCTG 961
 Qy 901 CCCTGCGGAGTGGCTGTGTAATCTACAGAGCGCACTTCTTCTACTTTTATAGATG 960
 Db 960 CCCTGCGGAGTGGCTGTGTAATCTACAGAGCGCACTTCTTCTACTTTTATAGATG 901
 Qy 961 ACCTATCCAGAGGAGGCTTACCCGACGAAGAAGACACCGCCCCCGCAGCCATCTTGGCCAG 1020
 Db 900 ACCTGCGGAGGAGGCTTACCCGACGAAGAAGACCGCCCCCGCAGCCATCTTGGNAAC 841
 Qy 1021 ATCTCCGCGCGCCCGCTGGCTGCTCCACCC-----CGCCACCGCTACCGTTGAGA 1074
 Db 840 ATCTCCGCGGAGAGACCATATTTGGGACACACCGCCCTTCAGAAAACGTTACAGATGCGC 781
 Qy 1075 AGGAAAATGGCATCTTCAACACCGCTCTCCGCGACCTTCGATATATCTGTCAAGGCT 1134
 Db 780 CGAAAGACGGGTATCTTCAATTCGCGCTTCTTACAGAAATTTGTACTCACAATAAAGGA 721
 Qy 1135 ACCACAGTCAGAACGCGCTCTCTGGGGGTGGACATGATGAGATTTTAAATTTGACGACTT 1194
 Db 720 G---GATACTCGGAGCCATCTTGGAAATGTTAACTACCTCAATTCACATCGGCCAGTTC 664
 Qy 1195 GTTCCCGCGGAGGGGACCAAAATCTTATACCTTTGAAATCTACAGAAATAGA 1254
 Db 664 CTCCCGCTCTCAGCGGACCAACCCCTTACCTTTTCCAATACTACCGTATTAGA 604
 Qy 1255 AAGGTTAAGGTTGAAATCTTGGCCCTGCTCCCGCATCACCGGGGTGATAGGGAGTGGGC 1314
 Db 603 AAGGTTAAGGTTGAAATCTTACCCGAGAGACCCCATCACCTCTTAATCAAGAGGTGTTGGG 544
 Qy 1315 TCCACTGCTCTTATCTTAGATGATACTTTGTAAAGGCGCCACAGCCCTTAAACCTATGAC 1374
 Db 543 TCCACTGCTCTTATCTTGGATGCCACTTTGTAAACCCCTCCACCACTTTGGGCTATGAC 484
 Qy 1375 CCATATGATAACTTCTCTCCCGCATCAATCCCCCAACCCCTTCTCTACAGCTCCCGT 1434
 Db 483 CCCTATATTAATACTCTCTCCCGCATCAATCAATAGGCGAGCCCTTTTACTCCTCAGG 424
 Qy 1435 TACTTCACACCCAAACCTGTTCTGACTCCACATTTGATTTACTTCCAAACCAATAACAA 1494
 Db 423 TACTTCACCCCAACCTGAGCTGGACCAAAACAAATGATTTGGTTTCCACCAATATATAA 364

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Qy	1195	GTTCCTCCCGGAGGGGGACCAACAAATCTCTATACCCCTTTGAATACTACAGAAATAAGA	1254
Db	476	CTCCCCCTCAGGCGGCACCAACCCCTACCCCTACCTTTCCAATACTACCGTATTAGA	417
Qy	1255	AAGTTAAGGTTGNAATTTCTGGCCCTGCTCCGCCATCACCCAGGGTGATAGGGGAGTGGGC	1314
Db	416	AAGGCTAAATATGAATTTTACCCAGAGACCCCATCACCTCTAATCAAGAGGGTGTGGG	357
Qy	1315	TCCACTGCTGTATTCTAGATGATACTTTGTAAAGGCCACAGCCCTAACCTATGAC	1374
Db	356	TCCACTGTTGTTATCTTGGATGCCAATTTGTAAACCCCTCCACCAACTTGGCCTATGAC	297
Qy	1375	CCATATGTAAACTACTCTCCCGCCATACAATCCCCCAACCCCTTCTCCTACCACTCCCGT	1434
Db	296	CCCTATATTAACTACTCTCCCGCCACACCAATAAGGCAGGCCCTTTACCTACCACCTCCAGG	237
Qy	1435	TACTTCACACCCAAACCTGTTCTTGACTCCACCATTGATTACTTCCAAACCAATACAAA	1494
Db	236	TACTTCACCCCAACCTGAGCTGGACCAACAAATTGATTGGTTCCACCCCAATATAAA	177
Qy	1495	AGGAATCAGCTTTGGAT	1511
Db	176	AGAAACCAGCTGTGGCT	160

Search completed: August 5, 2005, 02:42:15
Job time : 987 secs

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OM nucleic - nucleic search, using sw model

Run on: August 4, 2005, 23:27:58 ; Search time 7724 Seconds
(without alignments)
11122.618 Million cell updates/sec

Title: US-10-808-964A-2
Perfect score: 1773
Sequence: 1 ggtactctcggtgattgttc.....caaatcgcccttcgggtacc 1773

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sta.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	1386.4	78.2	1768	14 AF264042	Porcine c
C 2	1378.4	77.7	1768	14 AF264040	Porcine c
C 3	1370.4	77.3	1768	14 AF264039	Porcine c
C 4	1370.4	77.3	1768	14 AF520783	Porcine c
C 5	1370.4	77.3	1768	14 AF544024	Porcine c
C 6	1368.8	77.2	1768	14 AF264041	Porcine c
C 7	1367.2	77.1	1768	14 AF264038	Porcine c
C 8	1364	76.9	1768	14 AF264043	Porcine c
C 9	1364	76.9	1768	14 AF454546	Porcine c
C 10	1357.6	76.6	1768	14 AF201309	Porcine c
C 11	1346.4	75.9	1768	14 AF201305	Porcine c
C 12	1346.4	75.9	1768	14 AF201308	Porcine c
C 13	1343.2	75.8	1768	14 AF201306	Porcine c
C 14	1341.6	75.7	1768	14 AF201310	Porcine c
C 15	1340	75.6	1768	14 AF201307	Synthetic
C 16	1306	73.7	1767	12 AJ623306	Synthetic
C 17	1304.4	73.6	1767	14 AF201311	Porcine c
C 18	1303.4	73.5	1767	14 AY122275	Porcine c
C 19	1301.2	73.4	1767	14 AY288134	Porcine c

C 20	1296.4	73.1	1767	14 AY294310	Porcine c
C 21	1288.4	72.7	1767	14 AY288133	Porcine c
C 22	1285.2	72.5	1768	6 AX379562	Sequence
C 23	1285.2	72.5	1768	14 AY099498	Porcine c
C 24	1278.8	72.1	1768	6 AX379560	Sequence
C 25	1278.8	72.1	1768	14 AY099496	Porcine c
C 26	1277.2	72.0	1768	6 AX379564	Sequence
C 27	1277.2	72.0	1768	14 AY099500	Porcine c
C 28	1274	71.9	1768	6 AX379561	Sequence
C 29	1274	71.9	1768	6 AX379563	Sequence
C 30	1274	71.9	1768	14 AY099495	Porcine c
C 31	1274	71.9	1768	14 AY099499	Porcine c
C 32	1262.6	71.2	1759	14 PCCOMGEN	Porcine chr
C 33	1261.4	71.1	1768	14 AF305532	Porcine c
C 34	1261.4	71.1	1768	14 AF305533	Porcine c
C 35	1252	70.6	1762	6 AX379559	Sequence
C 36	1252	70.6	1762	14 AY099497	Porcine c
C 37	1218.2	68.7	1759	6 AX379565	Sequence
C 38	1218.2	68.7	1759	14 AY099501	Porcine c
C 39	1196.8	67.5	7400	6 AX226286	Sequence
C 40	1195.8	67.4	5225	6 AX226280	Sequence
C 41	1195.8	67.4	5650	6 AX226281	Sequence
C 42	1059.8	59.8	1759	6 A97282	Sequence 5
C 43	1059.8	59.8	1759	6 AR145612	Sequence
C 44	1059.8	59.8	1759	6 CQ768117	Sequence
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ALIGNMENTS

RESULT 1
AF264042/c
LOCUS Porcine circovirus type 2 isolate 40895 complete genome.
DEFINITION Porcine circovirus type 2 isolate 40895 complete genome.
ACCESSION AF264042
VERSION AF264042.1 GI:9392644
SOURCE Porcine circovirus 2
ORGANISM Porcine circovirus 2
KEYWORDS Viruses; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE 1 (bases 1 to 1768)
AUTHORS Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
TITLE Genetic characterization of type 2 porcine circovirus (PCV-2) from pigs with postweaning multisystemic wasting syndrome in different geographic regions of North America and development of a differential PCR-restriction fragment length polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2
J. Clin. Microbiol. 38 (7), 2494-2503 (2000)

JOURNAL MEDLINE 20341537
PUBMED 10878032
REFERENCE 2 (bases 1 to 1768)
AUTHORS Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-2000) VMRCVM, Virginia Tech, 1410 Prices Fork Road, Blacksburg, VA 24061, USA
FEATURES
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ORIGIN

Query Match 78.2%; Score 1386.4; DB 14; Length 1768;
Best Local Similarity 90.3%; Pred.No. 0;
Matches 1543; Conservative 0; Mismatches 146; Indels 19; Gaps 5;
QY 3 TACCTCCGTGGATTGTTCTCCAGCAGTCTTCCAAAATTGCAAGTAGTAATCCTCCGATA 62
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DB 1643 GAGAGCTTCTACAGCTGGGACAGCAGTGTGAGGAGTACCATTCCAAACGGGGTCTGATTGCT 1584
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QY 1610 ATGTACAATCAGAGAATTTAATCTTAAAGACCCCGCACTTAAACCTTAAATGAATAAAA 1669
DB 86 ATGTACAATCAGAGAATTTAATCTTAAAGACCCCGCACTTAAACCTTAAATGAATAAAA 30
QY 1670 ATAAAAACCATTCAGATGATGATAACAA 1697
DB 29 ATAAAAACCATTCAGAGTGTATAAAAA 2

RESULT 2
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LOCUS AF264040 1768 bp DNA linear VRL 23-JUL-2000
DEFINITION Porcine coronavirus type 2 isolate 10489 complete genome.
ACCESSION AF264040

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Db 326 ATGACCCATATGTAACACTTCTCCGCGCATACAAATCCCGCCCTTCTTCTTACCACT 267
Qy 1430 CCGGTACTTCCACACCCCAAACTGTTCTTGACTCCACCAATGATTACTTCCAAACCAATA 1489
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Qy 1610 ATGTACAAATCAGAGAAATTTAATCTTAAAGACCCCACTTAAACCTTAAATGAATAAA 1669
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Qy 1670 ATAAAAACCATACGATGTGATAACAA 1697
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LOCUS Porcine circovirus type 2 isolate 26607 complete genome. 1768 bp DNA linear VRL 23-JUL-2000
DEFINITION Porcine circovirus type 2 isolate 26607 complete genome.
ACCESSION AF264039
VERSION AF264039.1 GI:9392635
KEYWORDS
SOURCE Porcine circovirus 2
ORGANISM Porcine circovirus 2
REFERENCE 1 (bases 1 to 1768)
Virus; ssDNA viruses; Circoviridae; Circovirus.
Fenaux,M., Halbur P.G., Gill,M., Toth,T.E. and Meng,X.J.
TITLE Genetic characterization of type 2 porcine circovirus (PCV-2) from pigs with postweaning multisystemic wasting syndrome in different geographic regions of North America and development of a differential PCR-restriction fragment length polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2
J. Clin. Microbiol. 38 (7), 2494-2503 (2000)
JOURNAL 20341537
MEDLINE 10878032
PUBMED
REFERENCE 2 (bases 1 to 1768)
Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
AUTHORS Direct Submission
TITLE Submitted (08-MAY-2000) VNRVCM, Virginia Tech, 1410 Prices Fork Road, Blacksburg, VA 24061, USA
JOURNAL Location/Qualifiers
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ORIGIN
Query Match 77.3%; Score 1370.4; DB 14; Length 1768;
Best Local Similarity 89.8%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 156; Indels 19; Gaps 5;
Qy 3 TACCTCCGTGGATGTTCTCCAGCAGTCTTCCAAAATTTGCAAGTAGTAATCTCCGATA 62
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Db	626	GGAGAGGAAATAATGGCATCTTCAACACCCGCTCTCTCCGCACTTTCGGATATCTGTCA	567
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QY	1310	TGGGCTCCACTGCTGTTATCTAGATGATGATGATGATGATGATGATGATGATGATG	1369
Db	386	TGGGCTCCACTGCTGTTATCTAGATGATGATGATGATGATGATGATGATGATGATG	327
QY	1370	ATGACCCATATGAACTACTCTCTCCGCCATCAATCCCAACCTCTCTCTACCACT	1429
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QY	1430	CCCGTTACTTCAACCCAAACCTGTTTGTGACTCCACCAATGATTAATTTCCAAACCAATA	1489
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Db	206	ACAAAAGGATCAGCTTTGGATGAGGCTACAAACCTCTAGAAATGTGACCACTAGGCC	147
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Db	29	ATAAAAACGATTCAGATGTGATAACAA	2
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AF520783/c			
LOCUS			
1768 bp DNA linear VRL 08-JUL-2002			

DEFINITION Porcine circovirus type 2 isolate JHP, complete genome.

ACCESSION AF520783

VERSION AF520783.1 GI:21702689

KEYWORDS Porcine circovirus 2

SOURCE Porcine circovirus 2

ORGANISM Viruses; ssDNA viruses; Circoviridae; Circovirus.

REFERENCE 1 (bases 1 to 1768)

AUTHORS Park,J.H., Roh,I.S., Song,J.Y., Cha,S.H. and Choi,E.J.

TITLE Direct Submission

JOURNAL Submitted (07-JUN-2002) Virology Division, National Veterinary Research and Quarantine Service, Anyang 6-Dong, Anyang, Gyeonggi 430-824, Korea

FEATURES

source

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Query Match 77.3%; Score 1370.4; DB 14; Length 1768;

Best Local Similarity 89.8%; Pred. No. 0;

Matches 1533; Conservative 0; Mismatches 156; Indels 19; Gaps 5;

QY 3 TACCTCCGTGGATTGTTCTCCAGCAGTCTTCCAAAATTGCAAGTAGTAATCCTCGATA 62

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 DEFINITION AF544024
 ACCESSION AF544024.1 GI:23267184
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 SOURCE Porcine circovirus 2
 ORGANISM Porcine circovirus 2
 Viruses; ssDNA viruses; Circoviridae; Circovirus.
 REFERENCE 1 (bases 1 to 1768)
 Kim, K.M., Song, Y.K., Park, H.S. and Kang, S.Y.
 TITLE Characterization of porcine circovirus type 2 isolated in Korea
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1768)
 Kim, K.M., Song, Y.K., Park, H.S. and Kang, S.Y.
 AUTHORS Direct Submission
 TITLE Submitted (08-SEP-2002) College of Veterinary Medicine, Chungbuk
 JOURNAL National University, #48, Gaehin-dong, Heungduk-Ku, Cheongju
 361-763, Korea
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DEFINITION Porcine circovirus type 2 isolate 40856 complete genome.
ACCESSION AF264041
VERSION AF264041.1 GI:9392641
KEYWORDS
SOURCE Porcine circovirus 2
ORGANISM Porcine circovirus 2
REFERENCE 1 (bases 1 to 1768)
AUTHORS Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
TITLE Genetic characterization of type 2 porcine circovirus (PCV-2) from pigs with postweaning multisystemic wasting syndrome in different geographic regions of North America and development of a differential PCR-restriction fragment length polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2
J. Clin. Microbiol. 38 (7), 2494-2503 (2000)
MEDLINE 20341537
PUBMED 10878032
REFERENCE 2 (bases 1 to 1768)
AUTHORS Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.

TITLE Direct Submission
 JOURNAL Submitted (08-MAY-2000) VMRCUM, Virginia Tech, 1410 Prices Fork Road, Blacksburg, VA 24061, USA
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 Best Local Similarity 89.7%; Pred. No. 0;
 Matches 1532; Conservative 0; Mismatches 157; Indels 19; Gaps 5;
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LOCUS Porcine circovirus type 2 isolate 26606 complete genome.
DEFINITION Porcine circovirus type 2 isolate 26606 complete genome.
ACCESSION AF264038
VERSION AF264038.1 GI:9392632
KEYWORDS
SOURCE Porcine circovirus 2
ORGANISM Porcine circovirus 2
VIRUSES; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE 1 (bases 1 to 1768)
Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
Genetic characterization of type 2 porcine circovirus (PCV-2) from
pigs with postweaning multisystemic wasting syndrome in different
geographic regions of North America and development of a
differential PCR-restriction fragment length polymorphism assay to
detect and differentiate between infections with PCV-1 and PCV-2
J. Clin. Microbiol. 38 (7), 2494-2503 (2000)
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REFERENCE 2 (bases 1 to 1768)
Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
Direct Submission
Submitted (08-MAY-2000) VMRCVM, Virginia Tech, 1410 Prices Fork
Road, Blacksburg, VA 24061, USA
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Query Match 77.1%; Score 1367.2; DB 14; Length 1768;
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DEFINITION Porcine circovirus type 2 isolate 34464 complete genome.
ACCESSION AF264043
VERSION AF264043.1 GI:9392647
KEYWORDS Porcine circovirus 2
SOURCE Porcine circovirus 2
ORGANISM Porcine circovirus 2
VIRUSES; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE 1 (bases 1 to 1768)
AUTHORS Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
TITLE Genetic characterization of type 2 porcine circovirus (PCV-2) from pigs with postweaning multisystemic wasting syndrome in different geographic regions of North America and development of a differential PCR-restriction fragment length polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2
JOURNAL J. Clin. Microbiol. 38 (7), 2494-2503 (2000)
MEDLINE 20341537
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REFERENCE 2 (bases 1 to 1768)
AUTHORS Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-2000) VMRCUM, Virginia Tech, 1410 Prices Fork Road, Blacksburg, VA 24061, USA
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ACCESSION AF454546
VERSION AF454546.1 GI:18071939
KEYWORDS
SOURCE Porcine circovirus 2
ORGANISM Porcine circovirus 2
VIRUSES; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE 1 (bases 1 to 1768)
AUTHORS Kim, K.M., Kim, D.Y., Park, H.S., Song, Y.K. and Kang, S.Y.
TITLE Cloning and sequencing of porcine circovirus type 2 isolated in Korea
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1768)
AUTHORS Kim, K.M., Kim, D.Y., Park, H.S., Song, Y.K. and Kang, S.Y.
TITLE Direct Submission
JOURNAL Submitted (02-DSC-2001) College of Veterinary Medicine, Chungbuk National University, 48 Gaeshin-dong, Heungduk-ku, Cheongju 361-763, Korea
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DEFINITION	AF201309				
ACCESSION	AF201309.1	GI:7021355			
VERSION					
KEYWORDS	Porcine circovirus 2				
SOURCE	Porcine circovirus 2				
ORGANISM	Viruses; ssDNA viruses; Circoviridae; Circovirus.				
REFERENCE	1 (bases 1 to 1768)				
AUTHORS	Mankertz, A., Domingo, M., Folch, J. M., LeCann, P., Jestin, A., Segales, J., Chmielewicz, B., Plana-Duran, J. and Soike, D.				
TITLE	Characterisation of pcv-2 isolates from Spain, Germany and France				
JOURNAL	Virus Res. 66 (1), 65-77 (2000)				
MEDLINE	20120936				
PUBMED	10653918				
REFERENCE	2 (bases 1 to 1768)				
AUTHORS	Mankertz, A., Domingo, M., Folch, J. M., LeCann, P., Jestin, A., Segales, J., Chmielewicz, B., Plana-Duran, J. and Soike, D.				
TITLE	Direct Submission				
JOURNAL	Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer 20, Berlin 13353, Germany				
FEATURES	Location/Qualifiers				

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Qy	363 GCCCACTATGACGTGTACAGCTGTCTTCTCCAAATCACGCTGTGCAATCTTCGCGTCACTTT 422	
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Qy	423 CAAAGTTTCAGCCAGCCCGCGGAAATTTCTCACAATAGTTTACAGGAAATGTCTCGGCTAC 482	
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DEFINITION Porcine circovirus type 2 isolate GER1, complete genome.
ACCESSION AF201305
VERSION AF201305.1 GI:7021343
KEYWORDS
SOURCE Porcine circovirus 2
ORGANISM Porcine circovirus 2
VIRUSES; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE 1 (bases 1 to 1768)
AUTHORS Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A., Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.
TITLE Characterisation of PCV-2 isolates from Spain, Germany and France
JOURNAL Virus Res. 66 (1), 65-77 (2000)
MEDLINE 20120936
PUBMED 10653918
REFERENCE 2 (bases 1 to 1768)
AUTHORS Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A., Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordrufer 20, Berlin 13353, Germany
FEATURES
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Porcine circovirus 2
Viruses; ssDNA viruses; Circoviridae; Circovirus.
1 (bases 1 to 1768)
Mankertz,A., Domingo,M., Polch,J.M., LeCann,P., Jestin,A.,
Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.
Characterisation of PCV-2 isolates from Spain, Germany and France
Virus Res. 66 (1), 65-77 (2000)
20120936
10653918
2 (bases 1 to 1768)
Mankertz,A., Domingo,M., Polch,J.M., LeCann,P., Jestin,A.,
Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.
Direct Submission
Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer 20,
Berlin 13353, Germany
Location/Qualifiers
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Query Match

75.8%; Score 1343.2; DB 14; Length 1768;

Best Local Similarity 88.8%; Pred. No. 0; Matches 1516; Conservative 0; Mismatches 173; Indels 19; Gaps 5;			
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Qy	63	GAGAGCTTCTACAGCTGGGACGACGATTTGAGGAGTACCATCTCTGGGGGGCTGTATGCT	122
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Porcine circovirus type 2 isolate SPA3, complete genome.

AP201310.1 GI:7021358

Porcine circovirus 2

Porcine circovirus 2

Viruses; ssDNA viruses; Circoviridae; Circovirus.

1 (bases 1 to 1768)

Mankertz, A., Domingo, M., Folch, J. M., LeCann, P., Jestin, A.,

Segales, J., Chmielewicz, B., Plana-Duran, J. and Soike, D.,

Characterisation of PCV-2 isolates from Spain, Germany and France

Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer 20,

Berlin 13353, Germany

Location/Qualifiers

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ORIGIN

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VERSION	AF201307.1	GI:7021349	
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SOURCE	Porcine circovirus 2		
ORGANISM	Porcine circovirus 2		
REFERENCE	Viruses; ssDNA viruses; Circoviridae; Circovirus.		
AUTHORS	1 (bases 1 to 1768)		
TITLE	Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A., Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.		
JOURNAL	Characterisation of PCV-2 isolates from Spain, Germany and France		
MEDLINE	Varus Res. 66 (1), 65-77 (2000)		
PUBMED	20120936		
REFERENCE	10653918		
AUTHORS	2 (bases 1 to 1768)		
TITLE	Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A., Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.		
JOURNAL	Direct Submission		
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